# us-09-768-826-47\_copy\_24\_105.rpr

SEQ 12 NO: 47 (24-105) QQ) Page 1 AC NO: S17449; Database; PIR-73

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

using sw model protein search, OM protein April 28, 2003, 14:38:11; Search time 17.7526 Seconds (without alignments) 444.049 Million cell updates/sec Run on:

US-09-768-826-47\_COPY\_24\_105 427

1 EDNDEFFMDFLQTLLVGTPE........VQVLGSQDGAGTDYKDDDDK 82 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable ligand-bi	polychlorinated bi	. Clara cell 10K pro	FHG22 protein prec	uteroglobin precur	uteroglobin precur	probable polyketid	fibronectin-bindin	t7i23.15 protein -	cell specific 10K	BNI1 protein - yea	hypothetical prote	mannose-6-phosphat	uteroglobin precur	iron(III)-binding	outer surface prot		probable RNA-bindi	phosphodiesterase	exoribonuclease, v		MG331 homolog P01_	g	_	hypothetical prote		hypothetical prote	E	H+-transporting AT
SUMMARIES	QI	S17449	A36581	JS0036	S68231	UGRB	UGMS	T17420	C86790	T38128	JC2026	S63244	S30947	S41122	UGRBL	AD3580	S70285	A71243	T38656	T30244	T30175	T30174	873690	B64175	G71146	E96641	043	B89808	XNRTY	C69395
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Asbaba
polychhorinated biphenyl-binding protein precursor - rat
polychhorinated biphenyl-binding protein precursor - rat
N;Alternate names: Clara cell 10K secretory protein
C;Species: Rattus norvegicus (Norway rat)
C;Species: Safetic Safe

	258         1 OYECHF         imidazoleglycerol-           258         2 B90982         imidazoleglycerol-           258         2 H85827         imidazoleglycerol-           362         2 A75208         sugar transport AT           84         2 D96730         uoknown protein F5           210         2 S69923         outer surface prot           744         2 A54901         long-chain-fatty-a           410         2 F75190         probable phosphono           1040         2 D81379         transmembrane effl	RESULT 1 S.1749 Probable ligand-binding protein RYD5 - rat C.Species: Rattus norvegicus (Norway rat) C.Date: 13-Jan-1995-#sequence_revision 13-Jan-1995 #text_change 05-Nov-1999	C. Racession: 3.1749.  EMBO J. 10, 2813-2819, 1991  A. Title: Novel genes for potential ligand-binding proteins in subregions of the olf A. Reference number: S17447; MUID:92007724; PMID:1915264  A. Reference number: S17449  A. Rocession: S17449  A. Rocession: S1744 Cobb.  A. Status: preliminary  A. Molecule type: MRNA  A. Residues: 1.94 Cobb.  A. Residues: 1.94 Cobb.  A. Residues: EMBL:X60661; NID:957735; PIDN:CAA43068.1; PID:957736
	14.6 25 14.6 25 14.6 25 14.6 36 14.6 88 14.5 21 14.5 74 14.4 4104	oinding pro	Accession: 31/44,7 Februs, 28. Dear, T.N.; Boehm, T.; Ke EMBO J. 10, 2813-2819, 1991 A.Title: Novel genes for po A.Title: Novel genes for po A. Seference number: 51747; A. Accession: 517449 A. Status: preliminary A. Molecule type: mRNA A. Mesedues: 1-94 < DEBA A. Cross-references: EMBL:X6
64 63 63 63 63 63	62.5 62.5 62.5 62.5 62.5 61.5 61.5	1 e ligand-k es: Rattus	C.ACCESSION: 31/44) EMBO J. 10, 2813-2819, A.Title: Novel genes f A.Reference number: S1A A.Accession: S17449 A.Accession: Treliminary A.Molecule type: mRNA A.Residues: 1.94 < CERA A.Residues: 1.94 < CERA A.Cross-references: EM
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		RESULT 1 S17449 probable 1i C; Species: C; Date: 13-	C) Acces R) Dear, EMBO J. A) Title A) Refer A) Acces A) Acces A) Resid A) Resid

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Gaps

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Length 94;

/ Match 67.9%; Score 290; DB 2; I Local Similarity 80.0%; Pred. No. 1.1e-24; es 56; Conservative 9; Mismatches 5;

Query Match Best Loc Matches ||||||| |LLVQVLDAQE 92 LLVQVLGSQD 70

61 83

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NAlternate names: blastokinin
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1980 #sequence_revision 15-Oct-1982 #text_change 15-Sep-2000
C;Accession: A92291; A93461; A90935; A24217; A90303; A90417; A33824; A94608; 146904;
R;Bahlly, A:; Atger, M:; Atger, P:; Cerbon, M:A:; Allzon, M:; Vu Hai, M:T:; Logeat, F
J: Biol. Chem. 258, 10384-10389; 1983
A;Tille: The rabbit uteroglobin gene. Structure and interaction with the progesterone
A;Reference number: A92391; MUID:83290960; PMID:6309802
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 376, 257-261, 1995
A:Title: Cloning of a Syrian hamster cDNA related to sexual dimorphism: establishment
A;Reference number: S68231; MUID:96105393; PMID:7498554
A;Accession: S68231
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A:Reference number: A90935; MUID:83157105; PMID:6299663
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R:Lopez de Haro, M.S.; Nieto, A.
FEBS Lett. 193, 247-249, 1985
A;Title: Primary structure of rabbit lung uteroglobin as deduced from the nucleotide A;Reference number: A24217; MUID:B6056319; PMID:2415398
A;Reference number: A24217
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                                                                                                                                                                                                                                                                                                                                                       C:Species: Mesocricetus auratus (golden hamster)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Aug-1998
C:Accession: S68231
                          27 FQRVIETLLMDTPSS-YEAAMELFSPDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIA 85
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Pred. No. 0.27;
9; Mismatches 20; Indels
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C;Superfamily: uteroglobin
F;1-21/Domain: signal sequence #status predicted
F;22-95/Product: FHG22 protein #status predicted
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A;Residues: 1-91 <BAI>
A;Cross-references: GB:K00049; NID:g165789
                                                                                                                                                                                                                                                                                                               FHG22 protein precursor - golden hamster
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Nucleic Acids Res. 11, 2257-2271, 1983
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ilarity 37.5%;
Conservative
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Best Local Similarity
Matches 18; Conserv
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A:Molecule type: mRNA
A:Residues: 1-95 <DOM>
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A; Residues: 22-91 <LOP>
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A; Residues: 1-91 <SUS>
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A; Molecule type: mRNA
A; Residues: 1-91 <CHA>
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                                                                                              GS 68
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N.Alternate names: urinary protein |
Cidra cert 1 Juk protein precursor - numan
CiSpecies: Homo suptiens (man)
Risingh G: Katyal: St.; Brown, W.E.; Philips, S.; Kennedy, A.L.; Anthony, J.; Squegli
Risingh G: Katyal: St.; Brown, W.E.; Philips, S.; Kennedy, A.L.; Anthony, J.; Squegli
Risingh G: Katyal: St.; Brown, W.E.; Philips, S.; Kennedy, A.L.; Anthony, J.; Squegli
Risingh G: Katyal: St.; Brown, W.E.; Philips, S.; Kennedy, A.L.; Anthony, J.; Squegli
Risingh G: Katyal: St.; Brown
Rise and CiSh G: St.
A. Accession: St. St.
A. Accession: Protein
A. Residues: 19-1 Lawerys; R.; Witters, R.; Gielens, C.; Soumillion, A.; Van De
CiBn. Chim. Acta 207, 239-249, 1992
A.; Residues: 22-43 - ReBP.
A. Residues: 13-91 - ReBP.
A. Residues: 13-91 - ReBP.
A. Residues: 13-91 - ReBP.
A. Residues: 1-91 - ReBP.
A. Residues: 1711 sprotein consists of two identical polypeptides linked by two disulfide E: Generics:
A;Residues: 1-18 <HAG>
A;Cross-references: EMBL:X51318; NID:g55536; PIDN:CAA35701.1; PID:g55537
Fibnland, T.C.; Svaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.
J. Mol. Biol. 224, 441-448, 1992
A;Title: Refined structure of rat clara cell 17 kDa protein at 3.0 A resolution.
A;Reference number: S21676; MUD:92219263; PMID:1560460
A;Contents: annotation, X-ray crystallography, 3.0 angstroms
C;Superfamily: uteroglobin
F:24/Disulfide bonds: interchain (to 90) #status experimental
F:90/Disulfide bonds: interchain (to 24) #status experimental
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C;Superfamily: uteroglobin
C;Superfamily: signal sequence #status predicted <SIG>
F;1-21/Domain: signal sequence #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 20.0%; Score 85.5; DB 2; Length 96; Best Local Similarity 35.5%; Pred. No. 0.029; Matches 22; Conservative 12; Mismatches 27; Indels
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; Pred. No. 0.12;
17; Mismatches 27;
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27.4%;
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Best Local
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A; Experimental source: lung
A; Note: sequence extracted from NCBI backbone (NCBIP:126148)
A; Note: parts of this sequence, including the amino end of the mature protein, were c
A; Note: parts of this sequence, including the amino end of the mature protein, were c
R; Margraf, Lr. R; Finegold, M.J.; Stanley, L.A.; Major, A.; Nawkins, H.K.; DeMayo, F.J
Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993
A; Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell
A; Reference number: I51925; MUID:94000840; PMID:8398159
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A;Title: Mouse Clara cell 10-kDa (CC10) protein: CDNA nucleotide sequence and molecul A;Reference number: A56656; MUID:93178380; PMID:8440203
A.Cross-references: GB:M32012; NID:g165807; PIDN:AAA31500.1; PID:g165809
R.Atger, M.; Perricaudet, M.; Tiollais, P.; Milgrom, E.
Blochem. Biophys. Res. Commun. 93, 1082-1088, 1980
A.Title: Bacterial cloning of the rabbit uteroglobin structural gene.
A.Tatile: Bacterial cloning of the rabbit uteroglobin structural gene.
A.Reference number: 146906, MUID: 80241888; PMID:6156676
A.Accession: 146906
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: MRN
A.Residues: 53-66, NT', 69-72 <AT2>
A.Consences: GB:M25038; NID:g165804; PIDN:AAA31499.1; PID:g165805
C.Comment: Uteroglobin is secreted by the uterus upon induction by progesterone. It b.
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A;Residues: 1-96 <STR>
A;Cross-references: GB:L24372; NID:9461147; PIDN:AAA65446.1; PID:9785054
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F.1-21/Domain: signal sequence #status experimental <SIG>
F.22-91/product: uteroglobin #status experimental <MAT>
F.24-Disulfide bonds: interchain (to 90) #status experimental
F.90/Disulfide bonds: interchain (to 24) #status experimental
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C;Complex: homodimer linked by two disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 19/1; 81/3
C;Complex: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin
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A; Residues: 1-96 <SIN>
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Matches 17; Conserv
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A; Residues: 1-96 <RES>
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 50-62;67-71 cP02>
R; Worlze, II; Surcouf, EI; Vaney, M.C.; Buehner, M.; Mornon, J.P.
Submitted to the Brookhaven Protein Data Bank, April 1989
A; Reference number: A50025; PDB:1UTG
A; Contents: annotation; X-ray crystallography, I:34 angstroms, residues 22-91
R; Mol. Biol. 194, 725-739, 1987
A; Title: Refinement of the C222-1 crystal form of oxidized uteroglobin at 1:34 angstroms
A; Reference number: A44652; MUID:88011213; PMID:356405
A; Contents: annotation; X-ray crystallography, I:34 angstroms
A; Reference number: A50553; PDB:2UTG
A; Contents: annotation; X-ray crystallography, I:64 angstroms, residues 22-91
A; Rally, R.; Delettre, J.
Submitted to the Brookhaven Protein Data Bank, May 1989
A; Contents: annotation; X-ray crystallography, I:64 angstroms, residues 22-91
B; Bally, R.; Delettre, J.
J; Mol. Biol. 206, 153-170, 1989
A; Contents: annotation; X-ray crystallography, I:64 angstroms; disulfide bonds
A; Reference number: A44653; MUID:89199637; PMID:2704039
A; Contents: annotation; X-ray crystallography, I:64 angstroms; disulfide bonds
B; Menne, C.; Suske, G.; Arnemann, J.; Wenz, M.; Cato, A.C.B.; Beato, M.
Proc. Natl. Acad. Sci. U.S.A. 79, 4853-4857, 1982
A; Title: Isolation and structure of the gene for the progesterone-inducible protein uter
A; Reference number: 146904
A; A; Reference number: 146904
A; A; Retenus; Lefalus; translated from GB/EMBL/DDBJ
                    A;Cross-references: GB:M27564; NID:g165792; PIDN:AAA31496.1; PID:g165793
A;Experimental source: lung
R;Atger, M.: Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E.
Blochem. J. 177, 985-988, 1979
A;Title: N-terminal sequences of uteroglobin and its precursor.
A;Reference number: A90303; MUID:79187160; PMID:571719
A;Accession: A90303
A;Molecule type: protein
A;Residues: 1-5,77,710,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10,77,10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 22-81,'Q',83-91 <PON>
R; Popp, R.A.; Foresman, K.R.; Wise, L.D.; Daniel Jr., J.C.
Proc. Natl. Acad. Sci. U.S.A. 75, 5516-5519, 1978
A; Title: Anino acid sequence of a progesterone-binding protein.
A; Reference number: A93824; MUID:79074850; PMID:281700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 22-49,'D',51,'EN',54-59,61-66,'NEPSL',72-91 <POP>
R;POPP, R.A.; Foresman, K.R.; Wise, L.D.; Daniel Jr., J.C.
submitted to the Atlas, October 1982
A;Reference number: A94608
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C;Accession: JC2026
R;Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; DeMayo, F.J.
Blochen. Blophys. Res. Commun. 197, 163-171, 1993
A;Title: Cloning and characterization of the mouse clara cell specific 10 kDa protein A;Reference number: JC2026; MUID:94071937; PMID:7916613
A;Accession: JC2026
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C;Comment: This protein is the major secretory product of the Clara cell'and binds
C;Superfamily: uteroglobin
F;73/Region: ochre stop codon
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A;Molecule type: DNA
A;Residues: 1-2100 <BAD>
A;Cross-references: EMBL:295334; PIDN:CAB08600.1; GSPDB:GN00066; SPDB:SPAC20GB.06
A;Experimental source: strain 972h-; cosmid c20G8
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C;Species: Mus musculus (house mouse)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
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                                                                                                                                                                                         2 DNDEFFM---DFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQP-MHKAE 57
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K; Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, May 1997

A; Reference number: 221772

A; Accession: T38128
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                          Length 540;
                                                                                                              37;
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                      DB 2;
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Best Local Similarity 33.3%; Pred. No. 73;
Matches 21; Conservative 12; Mismatches
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                 16.2%;
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Matches 22; Conserv
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A; Residues: 1-113 <RAY>
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probable polyketide synthase type I - Pseudomonas fluorescens
C; Species: T7420
R; Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E.
J. Bacteriol. 181, 2166-2174, 1999
A; Title: Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas flangement on muber: 218776; MUID: 99194726; PMID: 10094695
A; Title: Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas flangements: 17420
A; Reference number: 218776; MUID: 99194726; PMID: 10094695
A; Status: Prellminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1.2458 < NOW>
A; Residues: 1.2458 < NOW>
A; Residues: 1.2458 < NOW>
A; Residues: DNA
A; Residues: DLB
C; Genetics:
A; Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier protein
C; Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology < NATD:
F; 53-815/Domain: acyl carrier protein homology < ARPLP:
F; 1033-1446/Domain: acyl carrier protein homology < ARPLP:
F; 2337-2408/Domain: acyl carrier protein homology ARPLP:
F; 2337-2408/Domain: acyl carrier prote
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A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
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                                                                                                                                                                                                                                                                                                                DB 1; Length 96;
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C;Superfamily: uteroglobin
C;Keywords: lung; steroid binding; uterus
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-96/Product: uteroglobin #status predicted <AMI>
F;24/Disulfide bonds: interchain (to 90) #status predicted
F;90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                   Query Match 16.3%; Score 69.5; DE Best Local Similarity 30.6%; Pred. No. 1.6; Matches 19; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 16.3%; Score 69.5; D 11 Similarity 32.1%; Pred. No. 68; 17; Conservative 14; Mismatches
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A;Molecule type: DNA
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Gaps

RESULT 11

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mannose-6-phosphate isomerase (EC 5.3.1.8) - human
N;Alternate names: phosphomannose isomerase
C;Species: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: 07-Sep-1994 **Requence_revision 10-Nov-1995 **text_change 08-Oct-1999
C;Accession: $411.22; $38666
R;Proudfoot, A.E.I.; Turcatti, G; Wells, T.N.C.; Payton, M.A.; Smith, D.J.
Bur. J. Biochem. 219, 415-423, 1994
A;Title: Purification, cDNA cloning and heterologous expression of human phosphomanno
A;Reference number: $41122; MUID:94139717; PMID:8307007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A23825
F;Lopez de Haro, M.S.; Nieto, A.
Biochem. J. 235, 895-898, 1986
A;Title: Nucleotide and derived amino acid sequences of a cDNA coding for pre-uterogl
A;Reference number: A23825; MUD:86323069; PMID:3019311
A;Accession: A23825
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999 C;Accession: S30947; S28074
R;Luque, F; Mitchenall, L.A.; Chapman, M.; Christine, R.; Pau, R.N. Mol. Microbiol. 7, 447-459, 1993
A;Title: Characterization of genes involved in molybdenum transport in Azotobacter A;Reference number: S30947; MUID:93211287; PMID:8384683
A;Accession: S30947
A;Residues: 1-270 <LUQ>
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X76057; NID:9416016; PIDN:CAA53657.1; PID:9416017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:X69077; NID:949177; PIDN:CAA48819.1; PID:949178 C;Superfamily: molybdate-binding protein
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; Pred. No. 17;
14; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 2;
Pred. No. 10;
9; Mismatches 38
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Best Local Similarity 27.6%; Pred. No.
Matches 21; Conservative 14; Mismatc
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28.8%;
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VKRISQQAAAGNNMED 232
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Matches 19; Conserv
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A; Residues: 1-423 <PRO>
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A; Residues: 1-937, 74, 99-1429, °C', 1431-1953 <FRR>
A; Residues: 1-937, 74, 99-1429, °C', 1431-1953 <FRR>
A; Ricross-references: EMBL: L31766; NID: 9472524; PIDN: AAAA34455.1; PID: 9472525
B; Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.
submitted to the EMBL Data Library, October 1995
A; Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV A; Reference number: $60909
A; Accession: $60909
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A; Residues: 1.1553 <SEZ>
A; Residues: 1.253 <SEZ>
A; Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63225.1; PID:g1045237
A; Cross-references: EMBL:X92494; Nidedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A; Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from the Reference number: S65111; MUID:96310631; PMID:8740425
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A;Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63225.1; PID:g1045237
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
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4
                                                                                                  $63244
BNII protein - yeast (Saccharomyces cerevisiae)
N'Alternate names: protein N0646; protein YNL271c
C;Species: Saccharomyces cerevisiae
C;Spaces 27-Apr-1996 #feature-revision 03 May-1996 #text_change 23-Mar-2001
C;Accession: S63244; S63245; S46523; S60909; S55111
R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
Sh;Reference number: S63235
A;Reference number: S63235
A;Accession: S63244
A;Ancleule type: DAGA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 TLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDG- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 1 - Azotobacter vinelandii
C;Species: Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:BN11; SHE5; SYL39
A;Cross-references: SGD:S0005215; MIPS:YNL271c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1994 A; Description: Synthetic Lethals of CDC12. A; Reference number: $48524
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-1553 <SEN>
A; Cross-references: EMBL:271547; MIPS:YNL271c
A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 987-1953 <MES>
A;Cross-references: EMBL:271547; MIPS:YNL271c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain S288C R; Fares, H.F.; Pringle, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRAKKDYKDDSKK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 -- AGTDYKDDDDK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S63245
A; Accession: S63245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S65111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S48523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 2
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RESULT 12 S30947

ö g ò Q

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Cipecies: Brucella melitensis
Cipecies: Apides: Cipecies: Brucella melitens
Cipecies: Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD352; PMID:11756688
A;Accession: AD352; PMID:1175688
A;Accession: AD358
A;Accession: AD358
A;Accession: Brellatinary
A;Residues: 1-358
A;Cross-references: GB:AE008918; PIDN:AAL53807.1; PID:g17984739; GSPDB:GN00191
C;Genetics:
A;Gene: BMEI10565
A;Map position: II
A:Cross references: GB:M25609; NID:g164246; PIDN:AAA30960.1; PID:g164247
A:Experimental source: lung
C:Comment: Uteroglubuh. synthesized in the uterus and lung. is secreted by the uterus up
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung: steroid binding; uterus
F:1-21/Domain: signal sequence #status predicted <SIG>F:22-91/Product: uteroglobin #status predicted <MAT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iron(III)-binding periplasmic protein precursor BMEII0565 (imported) - Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.6%; Score 66.5; DB 1; Length 91; Best Local Similarity 25.8%; Pred. No. 3.3; Matches 16; Conservative 17; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
15.6%; Score 66.5; D
Best Local Similarity 31.4%; Pred. No. 16;
Matches 22; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GS 68
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Gaps

22; Indels 17; Length 358;

DB 2;

----- VKLLVQVL 66

a δ Search completed: April 28, 2003, 14:44:36 Job time : 18.7526 secs

| : | || G--EDKGFDY 209 67 GSQDGAGTDY 76

22 LYEGTLG-KYNVNEDAKAAMTELKSCIDGLQPMHKAEL----

## ACNO: 517449; Database: PIR-73 SER ID NO: 47 (2-105 as)

Page 1

April 28, 2003, 14:38:11; Search time 22.5155 Seconds (without alignments) 444.049 Million cell updates/sec Run on:

537 1 KGSRALLLVALTLFCICRMA......VQVLGSQDGAGTDYKDDDDK 104 US-09-768-826-47\_COPY\_2\_105 score: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 DB seq DB seq Minimum

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir2:\* pir3:\* pir4:\* pir1:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	probable ligand-bi	polychlorinated bi		protein p		uteroglobin precur	cell specific 10K	signal recognition			uteroglobin precur	probable RNA-bindi	mannose-6-phosphat	probable polyketid	fibronectin-bindin	t7i23.15 protein -	hypothetical prote			_	•	iron(III)-binding	outer surface prot		Se	3C3.20c protein -	phosphodiesterase	exoribonuclease, v	
SUM		S17449	A36581	JS0036	S68231	UGRB	UGMS	JC2026	S05197	S05198	S54143	UGRBL	T38656	S41122	T17420	G86790	T38128	S30947	T16137	S63244	T02269	C83075	AD3580	S70285	A43644	A71243	T10929	T30244	T30175	T30174
	DB	5	~	7	7	7	٦	7	~	7	7	1	~	7	~	~	7	~	~	~	7	7	7	7	7	7	7	7	7	c
	Length	94	96 .	91	95	91	96	113	504	504	. 504	91	609	423	2458	540	2100	270	299	1953	511	322	358	192	122	362	1321	1687	0	1719
æ	Query	64.2	18.0	17.1			•	14.6	14.2	14.2	14.2	•	13.6	. 13.1	12.9	12.8	12.8	•	12.6	12.6	12.5	12.4	•	•	12.2	•	•	12.2	12.2	12.2
	Score	344.5	96.5	92	98			78.5			76.5	92	73	•	69.5	69	68.5	68	٠	67.5	67		66.5	9			65.5		65.5	65.5
	Result No.	-	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

30	65	12.1	209	~	873690	MG331 homolog P01
31	65	12.1	255	~	B64175	repressor modE hom
32	65	12.1	312	~	G71146	hypothetical prote
33	65	12.1	842	7	E96641	hypothetical prote
34	65	12.1	2233	7	ZLNZP3	genome polyprotein
35	64.5	12.0	339	7	E90436	coA-ligase / coenz
36	64.5	12.0	403	7	B89808	hypothetical prote
37	64.5	12.0	454	٦	XNRTY	tyrosine transamin
. 38	64.5	12.0	518	7	H85440	cytochrome P450-li
39	64.5	12.0	882	Н	WMBEUS	gene UL5 protein -
40	64	11.9	190	7	T20725	hypothetical prote
41	64	11.9	342	ч	C69395	H+-transporting AT
42	64	11.9	627	7	н96951	fusion, PTS system
43	64	11.9	856	7	B71364	hypothetical prote
44	64	11.9	926	7	S30834	hypothetical prote
45	64	11.9	3187	7	JC5837	364K Golgi complex
					ALIGNMENTS	
RESULT 1 S17449						
probable	ligand	-bindin	g prote	in	probable ligand-binding protein RYD5 - rat	

C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

Gaps 64.2%; Score 344.5; DB 2; Length 94; llarity 75.0%; Pred. No. 2.1e-29; Conservative 11; Mismatches 11; Indels Ouery Match Best Local Similarity Matches 69; Conserv

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1 KGSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKA 60

2 KGSSA-LLVALTVLCICGLTRAEDDNEFFMEFLQTLLVGTPEELYEGPLGKYNVNDMAKA 60 q

οy

polychlorinated biphenyl-binding protein precursor - rat
N;Alternate names: Clara cell 10K secretory protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 0B-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 20-Aug-1999
C;Accession: A36581; S10185; S21676
K;Nordlund-Moeller, L.; Andersson, O.; Ahlgren, R.; Schilling, J.; Gillner, M.; Gusta
J. Biol. Chem. 265, 12690-12693, 1990
A;Title: Cloning, structure, and expression of a rat binding protein for polychlorina
A;Reference number: A36581; MUID:90324266; PMID:2115524

A; Accession: A36581

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-96 <NOR5
A;Residues: 1-96 <NOR5
A;Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040
A;Cross-references: GB:J05536; NLD:g206039; PIDN:AAA41817.1; PID:g206040
B;Hagen, G.; Wolf, M.; Katyal, S.L.; Singh, G.; Beato, M.; Suske, G.
Nucleic Acids Res. 18, 2939-2946, 1990
Nucleic Acids Res. 18, 2939-2946, 1990
A;Title: Tissue-specific expression, hormonal regulation and 5'-flanking gene region
A;Reference number: S10185; MUID:90272398; PMID:2349092

A;Status: translation not shown A;Molecule type: DNA

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uteroglobin precursor [validated] - rabbit.

N.Alternate names: blastokinin
C.Specias: Orytologus cuniculus (domestic rabbit)
C.Specias: Orytologus cuniculus (domestic rabbit)
C.Specias: Orytologus cuniculus (domestic rabbit)
C.Specias: 28-Feb-1980 #sequence_revision 15-Oct-1982 #text_change 15-Sep-2000
C.Accession: A92391; A93461; A90935; A24217; A90303; A90417; A93824; A94608; I46904;
F.Ballly, A.; Atger, M.; Atger, P.; Cerbon, M.A.; Alizon, M.; Vu Hal, M.T.; Logeat, F.
J. Biol. Chem. 258, 10384-10389; 1983
A/Tille: The rabbit uteroglobin gene. Structure and interaction with the progesterone
A/Reference number: A92391; MUID:83290960; PMID:6309802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               steady-state level and nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 376, 257-261, 1995
A;Title: Cloning of a Syrian hamster cDNA related to sexual dimorphism: establishment
A;Reference number: S68231; MUID:96105393; PMID:7498554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:K01657; NID:g165794; PIDN:AAA31497.1; PID:g165795
R:Lopez de Haro, M.S.; Nieto, A. FEBS Lett. 193, 247-249, 1985
A;Title: Primary structure of rabbit lung uteroglobin as deduced from the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:K00049; NID:g165789
R;Suske, G:; Wenz, M.; Cato, A.C.B.; Beato, M.
Nucleic Acids Res. 11, 2257-2271, 1983
A;Title: The uteroglobin gene region: hormonal regulation, repetitive elements
A;Reference number: A93461; MUID:83220783; PMID:6304644
A;Accession: A93461
                                                                                                                                                                                                                                                                                                                          FHG22 protein precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Aug-1998
C;Accession: S68231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KGSRALLLVALTLFC-----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KLSLCLLLVILAVHCYEANAANVC-PAVLSVSKSFLFDKV------EKFEAYLQTFN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:J00687; NID:g1772; PIDN:CAA25669.1; PID:g313668
R;Chandra, T.; Bullock, D.W.; Woo, S.L.C.
DNA 1, 19-26, 1981
4 AVTLTLVTLALCCSSASAEICPS-FQRVIETLLMDTPSS-YEAAMELFSPDQDMREAGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 95;
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A;Reference number: A90935; MUID:83157105; PMID:6299663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: uteroglobin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-95/Product: FHG22 protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 VNEDAKAAMTELKSCIDG-LQPMHKAELVKLLVQVLG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 86; DB 2; 30.9%; Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                              87
                                                                            65 LKSCIDGLQPMHKAELVKLLVQVLGS
                                                                                                                          62 LKKLVDTLPQKPRESIIKLMEKIAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: 266540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches .30; Conserv
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A; Residues: 1-91 <BAI>
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A; Residues: 1-91 <SUS>
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A; Residues: 1-91 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1.-95 < DOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A90935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Dominguez, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
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JS0036
Clara cell 10k protein precursor - human
NAlternate names: urinary protein 1
Clara cell 10k protein precursor - human
NAlternate names: urinary protein 1
Clara cell 10k protein names: urinary protein 1
Clara cell 10k protein names: urinary protein 1
Clara cell 10k protein names: urinary protein 1
Clara cell 10k plan 1
                                  A.Cross-references: EMBL:X51318; NID:955536; PIDN:CAA35701.1; PID:955537
R;Umland, T.C.; Swaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.
A;Umland, T.C.; Swaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.
A;Title: Netlined Structure of rat Clara cell 17 kDa protein at 3.0 A resolution.
A;Reference number: S21676; MUID:92219263; PMID:1560460
A;Reference number: S21676; MUID:92219263; PMID:1560460
C;Superfamily: uteroglobin
F;24/Disulfide bonds: interchain (to 90) #status experimental
F;90/Disulfide bonds: interchain (to 24) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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22-91/Product: Clara cell 10K protein "*status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 96.5; DB 2; Length 96; 29.8%; Pred. No. 0.0042; live 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 91; 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.8%
Matches 25; Conservative
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uteroglobin precursor - mouse
NiAlternate names: CC10, Clara cell 10K protein precursor; Clara cell secretory prote
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 21-Jan-1997 #text_change 22-Jun-1999
C;Accession: A53025; A56656; I51925; S24783
R;Stripp, B.R.; Huffman, J.A.; Bohinski, R.J.
Genomics 20, 27-35, 1994
A;Title: Structure and regulation of the murine Clara cell secretory protein gene.
A;Reference number: A33025; MUID:94292183; PMID:8020953
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A;Note: parts of this sequence, including the amino end of the mature protein, were C
R;Margraf, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Nawkins, H.K.; DeMayo, F.J
Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993
A;Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell
A;Reference number: I51925; MUID:94000840; PMID:8398159
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R;Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.
Exp. Lung Res. 19, 67-75, 1993
A;Title: Mouse clara cell 10-kDa (CC10) protein: CDNA nucleotide sequence and molecul A;Reference number: A56656; MUID:93178380; PMID:8440203
A;Accession: A56656
                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Residues: 55-66, NT', 69-72 <AT2>
A:Cross-references: GB:M25038; NID:g165804; PIDN:AAA31499.1; PID:g165805
C:Comment: Uteroglobin is secreted by the uterus upon induction by progesterone. It
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LALVTLALLCSPASAGICPR-----PAHVIENLLLGTPSS-YETSLKEFEPDDTMK 56
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A;Experimental source: lung
                                                                                                                                                            A; Cross-references: GB: M32012; NID: 9165807; PIDN: AAA31500.1; PID: 9165809
                                                                                                                                                                                  R;Atger, M.; Perricaudet, M.; Tiollais, P.; Milgrom, E. Biochem. Biophys. Res. Commun. 93, 1082-1088, 1980
A;Title: Bacterial cloning of the rabbit uteroglobin structural gene. A;Reference number: 146906; MUID:80241888; PMID:6156676
A;Accession: 146906
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F;24/Disulfide bonds: interchain (to 90) #status experimental
F;90/Disulfide bonds: interchain (to 24) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: homodimer; steroid binding; uterus F;1-21/Domain: signal sequence #status experimental <SIG>
                                                             Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Introns: 19/1; 81/3
C;Complex: homodimer linked by two disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AAMTELKSCIDGLQPMHKAELVKLLVQVLGS 90
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                                                                                A; Molecule type: DNA
A: Residues: 1-45, 'V', 47-91 <SU2>
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A; Residues: 1-96 <STR>
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A Medicance manager, A24217; MUID-86056319; PMID-2415398

A Moscasion, A22219; MID-86056319; PMID-2415398

A Medicanic 22-31, A2790; MID-2504; MID-150732; DINA AAN1496.1; PID-1515793

A Residence 22-31, A2790; MID-2504; MID-150732; DINA AAN1496.1; PID-1515793

A Medicanic and ASSOCIATION AND ASSOCIATI
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A;Title: Model for signal sequence recognition from amino-acid sequence of 54K subuni. A;Reference number: S05198; MUID:89330597; PMID:2502718
A;Accession: S05198
                          A; Accession: S10619
A; Molecule type: protein
A; Residues: 2-35; 58-70; 120-126; 141-153; 374-388; 416-426; 470-485 <BER>
C; Superfamily: signal recognition particle 54K protein
C; Keywords: GTP binding; nucleotide binding; P-loop
F; 1-504/Product: signal recognition particle 54K protein #status experimental <MAT>F; 108-115/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C.Accession: S05198 s14553
C.Accession: H.D.: Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter Nature 340, 482-486, 1989
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C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S54143
R;Patel, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X16319; NID:954193; PIDN:CAA34386.1; PID:954194
C;Superfamily: signal recognition particle 54k protein
F;2-504/Product: signal recognition particle 54k protein #status predicted
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A; Residues: 1-504 <PAT>
A; Cross-references: EMBL:X86373; NID:9784998; PIDN:CAA60132.1; PID:9784999
C; Superfamily: signal recognition particle 54K protein
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                                                                                                                                                                                                                                                         14.2%; Score 76.5; DE 32.4%; Pred. No. 3.6; Ive 16; Mismatches
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Pred. No. 3.6;
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R;Bernstain, H. EMBL Data Library, No
A;Reference number: S1453
A;Accession: S1453
A;Molecule type: mRNA
A;Residues: 1-42,'DV', 45-504 <BER2>
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32.4%;
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S54143
SRP 54 protein - human (fragment)
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Best Local Similarity 32.49
Matches 36; Conservative
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A; Residues: 1-504 <BER1>
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Best Local Similarity
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S05197

signal recognition particle 54K protein - dog

C; Species: Canis lupus familiaris (dog)

C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001

C; Accession: S05197; $10619

R; Roemisch, K.; Webb, J.; Herz, J.; Prehn, S.; Frank, R.; Vingron, M.; Dobberstein, B.

R; Roemisch, K.; Webb, J.; Herz, J.; Prehn, S.; Frank, R.; Vingron, M.; Dobberstein, B.

R; Roemisch, K.; Webb, J.; Herz, J.; Prehn, S.; Frank, R.; Vingron, M.; Dobberstein, B.

R; Reference number: S05197; MUID:89330596; PMID:2502717

A; Molecule type: mRNA

A; Residues: 1-504 <R0E>

A; Molecule type: mRNA

A; Residues: 1-504 <R0E>

A; Note: part of this sequence, including the amino end of the mature protein, was confir R; Bernstein, H.D.; Portizz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter, P.

R; Bernstein, H.D.; Portizz, M.A.; Strub, R.; Hoben, P.J.; Brenner, S.; Walter, P.

R; Reture 340, 482-486, 1989

A; Title: Model for signal sequence recognition from amino-acid sequence of 54K subunit characteric number: S05198; MUID:89330597; PMID:2502718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major secretory product of the Clara cell and binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coll Specific 10K protein - mouse
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Was musculus (house mouse)
CiAccession: JC2026
R;Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; DeNayo, F.J.
Biochem. Blophys. Res. Commun. 197, 163-171, 1993
A;Title: Cloning and characterization of the mouse clara cell specific 10 kDa paracession: JC2026
A;Reference number: JC2026; MUID:94071937; PMID:7916613
A;Recession: JC2026
A;Molecule type: DNA
A;Residues: 1-113 <RAY>
C;Comment: This protein is the major secretory product of the Clara cell and bic;Superfamily: uteroglobin
F;73/Region: ochre stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S ITITVVMLSICCSSASSDICPGFLQVLEALLMES-ESGYVASLKPFNPGSDLQNAGTQLK 63
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ALLLVALTLFCICRMATGEDND -- EFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAM 62
A;Cross-references: GB:L04503; NID:g202313; PIDN:AAA03625.1; PID:g433093
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                    DB 1; Length
                                                                  A introns: 19/1; 81/3

A introns: 19/1; 81/3

C;Complax: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin
C;Keywords: lung; steroid binding; uterus
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-96/Product: uteroglobin #status predicted <SIG>F;24/Oisulfide bonds: interchain (to 24) #status predicted
F;90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 78.5; DB 30.7%; Pred. No. 0.41; Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                    15.2%; Score 81.5; 26.2%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| :| | : ::|| TOLKELTEKILTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TELKSCIDGLQPMHKAELVKLLVQVLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCIDGLQPMHKAELVKLLVQVLGS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLVDTLPQETRINIMKLTEKILTS 87
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 26.29
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                    Query Match
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C;Accession: S41122; S38666
R;Proudfoot, A.E.I.; Turcatti, G.; Wells, T.N.C.; Payton, M.A.; Smith, D.J.
Eur. J. Blochem. 219, 415-423, 1994
A;Title: Purification, cDNA cloning and heterologous expression of human phosphomanno
A;Reference number: S41122; MUID:94139717; PMID:8307007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E.
J. Bacteriol. 181, 2166-2174, 1999
A;Title: Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas A;Reference number: Z18776; MUID:99194726; PMID:10094695
A;Accession: T17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: carrier protein
F; 31-429/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS1>
F; 35-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F; 959-1009/Domain: acyl carrier protein homology <ARCPI>
F; 1053-1446/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS2>
F; 2337-2408/Domain: acyl carrier protein homology <4CP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-2458 <NOW>
A;Cross-references: EMBL:AF081920; NID:g4582974; PID:g2781416; PIDN:AAC38075.1
                                                                                                                                                                                                                                                                                                                                                                                          mannose-6-phosphate isomerase (EC 5.3.1.8) - human N;Alternate names: phosphomannose isomerase C;Species: Homo sapiens (man) C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable polyketide synthase type I - Pseudomonas fluorescens
C;Species: Pseudomonas fluorescens
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C;Accession: T17420
                                                                                                                                      248 COMMPGMLLEONPOFLYDNPSIFVIGILNLPLKVSPVELYNEFSNHGHILGVAINQSINE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X76057; NID:g416016; PIDN:CAA53657.1; PID:g416017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 MAIALTPFOGLCGFRPVEE-----IVTFLKKVPE--FQFLIGDEAATHLKQTMSHDS 187
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                       ---GTLGKYNVNE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLVALTLF-CICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLG------KYNVNEDA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 423;
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                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAAMTELKSCIDGLOPMHK -- - AELVKLLVQVLGSQDGAGTDYKD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                       ---TPEELYE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 15q22-15qter
C; Superfamily: yeast mannose-6-phosphate isomerase
C; Reywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                              D----KAELVKLLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.1%; Score 70.5; D
Best Local Similarity 25.7%; Pred. No. 13;
Matches 27; Conservative 19; Mismatches
     ed. No. 10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:MPI
A;Cross-references: GDB:119397; OMIM:154550
  23.5%; Pred.
tive 20; Mis
                                                                               17 CRMATG --- EDNDEFFMDFLQTLLVG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%;
                             Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA A; Residues: 1-423 <PRO>
                             23;
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                                                                                                                                                                                                                                                      308
                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: blastokinin
C;Species: Lepus capensis (brown hare)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: A23825
R;Lopez de Haro, M.S.; Nieto, A.
Biochem. J. 235, 895-898, 1986
A;Title: Nucleotide and derived amino acid sequences of a cDNA coding for pre-uteroglobi
A;Reference-number: A23825
A;Molecule type: mRNA
A;Reston: A23825
A;Molecule type: mRNA
A;Restouce: Lung
C;Compan: Did (2,00)
A;Cross-references: GB:M25609; NID:g164246; PIDN:AAA30960.1; PID:g164247
A;Experimental source: Lung
C;Complex: homodimer linked by two disulfide bonds
C;Complex: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin, synthesized in the uterus
C;Complex: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin #status predicted <AMT>
F;1-21/Domain: signal sequence #status predicted <AMT>
F;2-91/Product: uteroglobin #status predicted
F;90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Schizosaccharomyces pombe (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe (C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T38656
R; Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, August 1997
A; Reference number: 221804
A; Reference number: 221804
A; Reference number: 221804
A; Reference number: 221804
A; Residues: preliminary: translated from GB/EMBL/DDBJ
A; Residues: 1-609 cMUR>
A; Residues: 1-609 cMUR>
A; Experimental source: strain 972h-; cosmid c343
                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                 Gaps
                                                                                                                           1 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable RNA-binding protein - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLVALTLFC-----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LALVILALLCSPASAGIC------PGFAHVIENLLLGTPSS-YGTSLKEFQPDDAMK
                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                    Length 504;
                                                                                                                                                                                                                                          56 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.2%; Score 76; DB 1; Length 91; Best Local Similarity 26.4%; Pred. No. 0.59; Matches 24; Conservative 17; Mismatches 34; Indels
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
                                                                               40;
                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                    Score 76.5; DE
Pred. No. 3.6;
                                                                         16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::| :| : | | : | | SAGMQMKKVLDTLPQTTRENIIKLTEKIVKS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAMTELKSCIDGLQPMHKAELVKLLVQVLGS 90
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                    14.2%;
32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.6%;
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   uteroglobin precursor - brown h
N;Alternate names: blastokinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 44/1; 96/2; 325/3
                                           Local Similarity
les 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: SPDB:SPAC343.07
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                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                           Best Loc
Matches
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R; Bolotin, A; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86790
A;Status: preliminary
A;Residues: 1-540 < STO>
A;Coss-references: GB:AE005176; PID:g12724308; PIDN:AAK05425.1; GSPDB:GN00146
A;Residues: 1-540 < STO>
A;Coss-references: GB:AE005176; PID:g12724308; PIDN:AAK05425.1; GSPDB:GN00146
C;Genetics: A;Gene: yngB
                                                                                                                                                                                                                                                                                                                                 fibronectin-binding protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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,
                                      Gaps
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                                                                                                 43 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.8%; Score 69; DB 2; Length 540; Best Local Similarity 30.6%; Pred. No. 24; Matches 22; Conservative 9; Mismatches 37; Indels
Best Local Similarity 32.1%; Pred. No. 1.2e+02;
Matches 17; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: G86790
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Search completed: April 28, 2003, 14:44:37 Job time: 23.5155 secs

80 LVKLLVQVLGSQ 91 :| |: || | 354 KLKQAVKFLGEQ 365

24 DNDEFFM---DFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQP-MHKAE 79

6 6 6

us-09-768-826-47.rpr

GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein April 28, 2003, 14:38:11; Search time 22.732 Seconds Run on:

(without alignments)
444.049 Million cell updates/sec

US-09-768-826-47

Perfect score:

542 1 MKGSRALLLVALTLFCICRM.....VQVLGSQDGAGTDYKDDDDK 105 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR\_73:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable ligand-bi		Clara cell 10K pro	in p	uteroglobin precur		uteroglobin precur	cell specific 10K	signal recognition	signal recognition	SRP 54 protein - h	probable RNA-bindi	mannose-6-phosphat	probable polyketid	fibronectin-bindin	t7i23.15 protein -	major allergen Fel	hypothetical prote	hypothetical prote		BNI1 protein - yea		iron(III)-binding	outer surface prot	major allergen cha	sarcocystatin A pr	probable maltose/m	3C3.20c protein -	phosphodiesterase
SUMMARIES	ΙD	S17449	A36581	JS0036	S68231 .	UGRB	UGMS	UGRBL	JC2026	S05197	805198	S54143	T38656	S41122	T17420	G86790	T38128	A56413	S30947	T16137	C83075	. S63244	T02269	AD3580	S70285	JC1136	A43644	A71243	T10929	T30244
	DB	7	7	7	~	П	-	Н	N	~	~	~	~	~	7	7	7	7	7	7	7	~	7	~	7	~	7	~	7	~
•	Query Match Length	94	96	91	95	91	96	91	113	504	504	504	609	423	2458	540	2100	92	270	299	322	1953	511	358	192	92	122	362	1321	1687
	Query	4.5	7.8	7.0	8.9	6.4	2.0	4.8	4.5	4.1	4.1			3.0				٠		2.5		2.5	2.4	2.3		2.1	2.1	2.1	2.1	2.1
op.	Ma	ف	-	-	٦ ·	Ä	H	Ä	Ä	Ä	<del>, i</del>	Ä	Н	7	-		7	_	П	-	_	_	П	-	Н	<del>1</del>	-	_	-	Н
	Score	349.5	96.5	92	91	68	81.5		ന	76.5	•	ö	73	70.5	69.5	9	68.5	68	9	67.5	•	67.5	9	66.5	99	65.5	65.5	65.5	65.5	65.5
	Result No.	1	7	m	4	S	ø	7	<b>ω</b>	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

prote repressor modE hom hypothetical prote hypothetical prote genome polyprotein coA-ligase / coenz hypothetical prote tyrosine transamin cytochrome P450-li probable DNA repai fusion, PTS system H+-transporting AT gene UL5 protein hypothetical prot exoribonuclease, exoribonuclease MG331 homolog E96641 ZLNZP3 E90436 B64175 G71146 H85440 B89808 WMBEU5 C69392 XNRTY 403 65.5 65.5 65 65 65 64.5 64.5 64.5 64.5 64 64 64 64 

### ALIGNMENTS

C; Species: Rattus norvegicus (Norway rat)
C; Date. 13-10-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999
C; Accession: S1749 # R; Reverne, E.B.; Rabbitts, T.H.
R; Dear, T.N.; Boohm, T.; Keverne, E.B.; Rabbitts, T.H.
R; Dear, T.N.; Boohm, T.; Keverne, E.B.; Rabbitts, T.H.
R; Perence of genes for potential ligand-binding proteins in subregions of the olface A; Reference number: S17447; MUID:92007724; PMID:1915264
A; Accession: S17449
A; Reference rugher mRNA
A; Residues: 1-94 < DEA> ä Gaps 1 MKGSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAK 60 A;Cross-references: EMBL:X60661; NID:g57735; PIDN:CAA43068.1; PID:g57736 DB 2; Length 94; Indels 64.5%; Score 349.5; DB 2 75.3%; Pred. No. 7.3e-30; tive 11; Mismatches 11 probable ligand-binding protein RYD5 - rat Conservative Best Local Similarity Matches 70; Conserv Query Match ò

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AAMTELKSCIDGLQPMHKAELVKLLVQVLGSQD 93 61 9 á a

Polychlorinated biphenyl-binding protein precursor - rat
N.Alternate names: Clara cell 10K secretory protein
C.Species: Rattus norvegicus (Norway rat)
C.Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 20-Aug-1999
C.Accession: A36581; S10185; S21676
R.Nordlund-Moeller, L.; Andersson, O.; Ahlgren, R.; Schilling, J.; Gillner, M.; Gusta
J. Biol. Chem. 265, 12690-12693, 1990
A;Title: Cloning, structure, and expression of a rat binding protein for polychlorina
A;Reference number: A36581; MUID:90324266; PMID:2115524

A; Accession: A36581

A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-96 <NOR>

A; Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040
R; Hagen, G.; Wolf, M.; Katyal, S.L.; Singh, G.; Beato, M.; Suske, G.
Wucleic Acids Res. 18, 2939-2946, 1990
A; Title: Tissue-specific expression, hormonal regulation and 5'-flanking gene region A; Reference number: S10185; MUD:90272398; PMID:2349092
A; Accession: S10185
A; Accession: S10185
A; Molecule type: DNA

Page

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N'Alternate names: blastokinin
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: A92291; A93461; A90335; A24217; A90303; A90417; A93824; A94608; I46904;
C;Accession: A92291; A93461; A90335; A24217; A90303; A90417; A93824; A94608; I46904;
R;Ballly', A:; Atger, M:; Atger, P:; Cerbon, M.A.; Alizon, M.; Vu Hai, M.T.; Logeat, F
J: Biol. Chem. 258, 10384-10389; 1983
A;Title: The rabbit uteroglobin gene. Structure and interaction with the progesterone
A;Reference number: A92391; MUID:83290960; PMID:6309802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett. 376, 257-261, 1995
A;Title: Cloning of a Syrian hamster CDNA related to sexual dimorphism: establishment
A;Reference number: S68231; MUID:96105393; PMID:7498554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Title: Hormonally regulated mammalian gene expression: steady-state level and nucle A/Reference number: A90935; MUID:83157105; PMID:6299663
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A;Cross-references: GB:K01657; NID:g165794; PIDN:AAA31497.1; PID:g165795
R;Lopez de Haro, M.S.; Nieto, A.
FBBS Lett. 193, 247-249, 1985
A;Title: Primary structure of rabbit lung uteroglobin as deduced from the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The uteroglobin gene region: hormonal regulation, repetitive elements and A; Reference number: A93461; MUID:83220783; PMID:6304644
A; Accession: A93461
                                                                                                                                                                                                                                                                                                                              FHG22 protein precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 15-Feb_1997 #sequence_revision 13-Mar-1997 #text_change 21-Aug-1998
                            50
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                            --- PSFORVIETLLMDTPSS-YEAAMELFS
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R;Chandra, T.: Bullock, D.W.; Woo, S.L.C.
DNA 1, 19-26, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :1-21/Domain: signal sequence #status predicted <SIG>:2-95/Product: FHG22 protein #status predicted <MAT>
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0.017;
                                                                                                                                      51 PDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIAQS 87
                                                                                        VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS 91
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R;Suske, G.; Wenz, M.; Cato, A.C.B.; Beato, M.
Nucleic Acids Res. 11, 2257-2271, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uteroglobin precursor [validated] - rabbit
                        MKLAVTLTLVTLALCCSSASAEIC ---
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Best Local Similarity 31.69
Matches 31; Conservative
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F;1-21/Domain: signal seque
F;22-95/Product: FHG?2 nro+
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A; Residues: 1-95 <DOM>
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A; Residues: 1-91 <BAI>
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A; Residues: 1-91 <SUS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S68231
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A;Residues: 1-18 cHAG>
A;Crosa-references: EMBL:X51318; NID:955536; PIDN:CAA35701.1; PID:955537
A;Crosa-references: EMBL:X51318; NID:955536; PIDN:CAA35701.1; PID:955537
J. Woll. Biol. 224, 441-448, 1992
A;Title: Refined structure of rat Clara cell 17 kDa protein at 3.0 A resolution.
A;Reference number: S21676; MUD:92219263; PMID:1560460
A;Contents: annotation, X-ray crystallography, 3.0 angstroms
C;Superfamily: uteroglobin
F;24/Disulfide bonds: interchain (to 90) #status experimental
F;90/Disulfide bonds: interchain (to 24) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.8%; Score 96.5; DB 2; Length 96; Best Local Similarity 29.8%; Pred. No. 0.0044; Matches 25; Conservative 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 92; DB 2; Length 91; 11arity 27.8%; Pred. No. 0.012; Conservative 18; Mismatches 36; Indels
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uteroglobin precursor - mouse
N;Alternate names: CCIO; Clara cell 10K protein precursor; Clara cell secretory prote
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 21-Jan-1997 #text_change 22-Jun-1999
C;Accession: A53025; A54056; I51925; S24783
R;Stripp, B.R.; Huffman, J.A.; Bohinski, R.J.
Genomics 20, 27-35, 1994
A;Title: Structure and regulation of the murine Clara cell secretory protein gene.
A;Reference number: A53025; MUID:94292183; PMID:8020953
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-96 <STR>
A; Cross-references: GB:L24372; NID:9461147; PIDN:AAA65446.1; PID:9785054
A; Cross-references: GB:L24372; NID:9461147; PIDN:AAA65446.1; PID:9785054
B; Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.
Exp. Lung Res. 19, 67-75, 1993
A; Title: Mouse Clara cell 10-kba (CC10) protein: cDNA nucleotide sequence and molecul A; Reference number: A56656; MUID:93178380; PMID:8440203
A; Accession: A56656
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A; Note: parts of this sequence, including the amino end of the mature protein, were of R; Margraf, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Nawkins, H.K.; DeMayo, F., Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993
A; Title: Cloning and tissue-specific expression of the cDNA for the mouse clara cell A; Reference number: IS1925; MUID:94000840; PMID:8398159
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 53-66, vNT', 69-72 <AT2>
A;Cross-references: GB:M25038; NID:9165804; PIDN:AAA31499.1; PID:9165805
C;Comment: Uteroglobin is secreted by the uterus upon induction by progesterone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                     A; residues: 1-45, V', 47-91 <SU2>
A;Cross-references: GB:M32012; NID:g165807; PIDN:AAA31500.1; PID:g165809
R;Atger, M.; Perricaudet, M.; Tiollais, P.; Milgrom, E.
Biochem. Biophys. Res, Commun. 93, 1082-1088, 1980
A;Title: Bacterial cloning of the rabbit uteroglobin structural gene. A;Reference number: I46906; MuID:80241888; PMID:6156676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKGSRALLLVALTLFC-----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA; protein
A;Residues: 1-96 <SIN>
A;Cross-references: EMBL:X67702; NID:g49690; PIDN:CAA47936.1; PID:g49691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: uteroglobin
C; Keywords: homodimer; steroid binding; uterus
F;1-21/Domain: signal sequence #status experimental <SIG>F;2-91/Product: uteroglobin #status experimental <MAT>F;24/Pisulfide bonds: interchain (to 90) #status experimental F;90/Disulfide bonds: interchain (to 24) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%; Score 89; DB 1; 27.8%; Pred. No. 0.026;
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                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS 91
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Best Local Similarity
Matches 27; Conserv
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A; Residues: 1-96 <RES>
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A; Contents: annotation; A: Tay crystallography, 1.64 angstroms; disulfide bonds
B; Menne, C.; Suske, G.; Arnemann, J.; Wenz, M.; Cato, A.C.B.; Beato, M.
Proc. Natl. Acad. Sci. U.S.A. 79, 4853-4857, 1982
A; Title: Isolation and structure of the gene for the progesterone-inducible protein uter
A; Reference number: I46904
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-91 cMRN>
A; Reference number: 146905; MUID: 81021016; PMID: 7417250
A; Accession: 146905
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 39-77 cCH2>
A; Molecule type: DNA
A; Residues: 39-77 cCH2>
A; CDSS-references: GB: M25057; NID: 9165802; PIDN: AA31498.1; PID: 9165803
B; Suske, G; Menne, C.; Cato, A; Wendz, M.; Beato, M.
Prog: Clin: Biol. Res: 85, 139-146, 1982
A; Title: Structure and regulated expression of the uteroglobin gene.
A; Reference number: 146907; MUID: 81275176; PMID: 6287481
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R:Morize. 1.5 Surcouf, E.; Vaney, M.C.; Epelboin, Y.; Buehner, M.; Fridlansky, F.; Milgr
Mol. Biol. 194, 725-739, 1987
J. Mol. Biol. 194, 725-739, 1987
A;Title: Refinement of the C222-1 crystal form of oxidized uteroglobin at 1.34 angstroms
A;Reference number: A44652; MUID:88011213; PMID:3656405
A;Contents: annotation; X-ray crystallography, 1.34 angstroms
R;Bally, R.; Delettre, J.
R;Bally, R.; Delettre, J.
R;Bally, R.; Delettre, J.
R;Bally, R.; Delettre, J.
Mol. Biol. 206, 153-170, 1989
A;Title: Structure and refinement of the oxidized P2-1 form of uteroglobin at 1.64 angst
A;Reference number: A44653; MUID:89199637; PMID:2704039
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-5, f*,7-10, x*,15,'G',17-54,'X',56,'B',58-66,'B',68-70,'XX',73 <ATG>
K;Ponstingl, H; Nieto, A; Beato, M.
Biochemistry 17, 3908-3912, 1978
                                                                             A;Molecule type: mRNA
A;Residues: 22-91 <LOP>
A;Cross-references: GB:M27564; NID:9165792; PIDN:AAA31496.1; PID:9165793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Amino acid sequence of progesterone-induced rabbit uteroglobin. A;Reference number: A90417; MUID:79042086; PMID:568483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 50-62;67-71 <PO2>
K; Morize, I.; Surcouf, E.; Vaney, M.C.; Buehner, M.; Mornon, J.P.
Submitted to the Brookhaven Protein Data Bank, April 1989
A; Reference number: A50025; PDB:1UTG
                                                                                                                                                                                                                                         RiAtger, M.; Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E. Bochem, J. 177, 985-988, 1979
A.Title: N-terminal sequences of uteroglobin and its precursor.
A;Reference number: A90303; MUID:79187160; PMID:571719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 22-81, 'Q', 83-91 <PON>
R; Popp, R.A.; Foresman, K.R.; Wise, L.D.; Daniel Jr., J.C.
Proc. Natl. Acad. Sci. U.S. 75, 5516-5519, 1978
A; Title: Amino acid sequence of a progesterone-binding protein.
A; Reference number: A93824; MUID: 79074850; PMID: 281700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A;Residues: 22-49, 'D',51,'EN',54-59,61-66,'NEPSL',72-91 <POP>
R;Popp, R.A.; Foresman, R.R.; Wise, L.D.; Daniel Jr., J.C.
Submitted to the Atlas, October 1982
Reference number: A24217; MUID:86056319; PMID:2415398
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                                           A;Accession: A24217
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14.1%; Score 76.5; Di
32.4%; Pred. No. 3.7;
iive 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      64 TELKSCIDGLQPMHKAELVKLLVQVLGS 91
                                                                                                                                                             14.5%;
                                                                                                                                                                                   Best Local Similarity 30.79
Matches 27; Conservative
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Best Local Similarity
Matches 36; Conserv
        A; Molecule type:
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S05198
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C'Species: Lepus capensis (brown hare)
C'Species: A3825
R'Lopez de Haro, M.S.; Nieto, A.
Blochen. J. 235, 895-898, 1986
A;Title. Nucleotide and derived amino acid sequences of a CDNA coding for pre-uteroglobi
A;Reference number: A23825, MUID:86323069; PMID:3019311
A;Reference number: A23825
A;Molecule type: mRNA
A;Residues: 1-91 <LOP>
A;Comment: Uteroglobin, synthesized in the uterus and lung, is secreted by the uterus up C;Complex: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin
C;Superfamily: uteroglobin status predicted <SIG>
F;22-91/Product: uteroglobin #status predicted <ANT>
E;24/Disulfide bonds: interchain (to 90) #status predicted
F;90/Disulfide bonds: interchain (to 24) #status predicted
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: JC2026
R:Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; DeMayo, F.J.
Biochem. Biophys. Res. Commun. 197, 163-171, 1993
A;Title: Cloning and characterization of the mouse clara cell specific 10 kDa protein of A;Reference number: JC2026; MUID:94071937; PMID:7916613
A;Accession: JC2026
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Cross-references: GB:L04503; NID:g202313; PIDN:AAA03625.1; PID:g433093
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                                          Aintrons: 19/1; 81/3
C;Complex: homodimer linked by two disulfide bonds
C;Superfamily: uteroglobin
C;Keywords: lung; steroid binding; uterus
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-96/Product: uteroglobin #status predicted <AMT>
F;24/Disulfide bonds: interchain (to 24) #status predicted
F;90/Disulfide bonds: interchain (to 24) #status predicted
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les 26: Conserv
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Signal recognition particle 54k protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-58p-1990 #text_change 23-Jul-1999
C;Accession: S05198; S14553
R;Bernstein, H.D.; Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter, P. Nature 340, 482-486, 1989
A;Title: Model for signal sequence recognition from amino-acid sequence of 54k subuni A;Reference number: S05198; MUID:89330597; PMID:2502718
A;Accession: S05198
A;Residues: 1-504 <-BRRL>
A;Cross-references: EMBL:X16319
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A. Residues: 1-504 <ROES
A. Cross-references: EMBL: X16318; NID:9928; PIDN:CAA34385.1; PID:9930
A. Cross-references: EMBL: X16318; NID:9928; PIDN:CAA34385.1; PID:9930
A. Note: part of this sequence, including the amino end of the mature protein, was con R. Bernstein, H.D.; Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter, P. Nature 340, 482-486, 1989
A. Title: Model for signal sequence recognition from amino-acid sequence of 54K subuni A. Reference number: S05198; MUID:89330597; PMID:2502718
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C; Date: 07-sep-1990 #sequence_revision 07-sep-1990 #text_change 02-Feb-2001
C; Accession: S05197; S10619
E; Roemisch, K.; Webb, J.; Herz, J.; Prehn, S.; Frank, R.; Vingron, M.; Dobberstein, B. Nature 340, 478-482, 1989
A; Title: Homology of 54K protein of signal-recognition particle, docking protein and A; Accession: S05197; MUID:89330596; PMID:2502717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 2-35;58-70;120-126;141-153;374-388;416-426;470-485 <BER>
C; Superfamily: signal recognition particle 54k protein
C; Keywords: GFP binding; nucleotide binding; P-loop
F;1-504/Product: signal recognition particle 54k protein #status experimental <MAT>
F;108-115/Region: nucleotide-binding motif A (P-loop)
'A; Residues: 1-13 <RAY>
C; Comment: This protein is the major secretory product of the Clara cell and binds C; Superfamily: uteroglobin
F; 73/Region: ochre stop codon
                                                                                                                                                                                                                                             ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                 2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                       6 ALLLVALTLFCICRMATGEDND--EFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY
                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                            ;;
                                                                                                                                                                     ; Score 78.5; DB
; Pred. No. 0.43;
15; Mismatches
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Length 504;

DB 2;

Score 76.5; DI Pred. No. 3.7; 16; Mismatches

Query Match
Best Local Similarity 32.4%;
Matches 36; Conservative 1

40; Indels

57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99

a ò g

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mannose-6-phosphate isomerase (EC 5.3.1.8) - human N;Alternate names: phosphomannose isomerase C;Species: Homo sapiens (man) C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999 C;Accession: S41122; S38666 F;Pursatti, G.; Wells, T.N.C.; Payton, M.A.; Smith, D.J. Eur. J. Biochem. 219, 415-423, 1994 A;Fitle: Purification, cDNA cloning and heterologous expression of human phosphomanno A;Reference number: S41122; MUID:94139717; PMID:8307007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: carrier protein
F:31-429/Domain: 3-oxoacyl-(acyl-carrier-protein) synthase I homology <0AS1>
F:35-815/Domain: [acyl-carrier-protein) S-malonyltransferase homology <AMT>
F:303-1009/Domain: acyl carrier-protein homology <ACP1>
F:1053-1446/Domain: 3-oxoacyl-(acyl-carrier-protein) synthase I homology <0AS2>
F:2337-2408/Domain: acyl carrier protein homology <ACP2>
                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas fluorescens
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C;Accession: T17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E. Bacteriol. 181, 2166-2174, 1999
A;Title: Characterization of the pyoluteorin biosynthetic gene cluster of A;Reference number: Z18776; MUID:99194726; PMID:10094695
A;Accession: T17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 MAIALTPFOGLCGFRPVEE-----IVTFLKKVPE--FOFLIGDEAATHLKQTMSHDS 187
                                                                                                                                               248 CQMMPGMILEQNPQFLYDNPSIFVIGILNLPLKVSPVELYNEFSNHGHILGVAINQSINE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X76057; NID:g416016; PIDN:CAA53657.1; PID:g416017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LLVALTLF-CICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLG------KYNVNEDA 59
                                                                                                   ----GTLGKYNVNE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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probable polyketide synthase type I - Pseudomonas fluorescens
                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                      27;
                                                                                                   ---TPEELYE--
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                                                                                                                                                                                                                                                         1 | | : ::||: : : | 308 DMTHYAEVAVSTYESCIEIIEKFHAIAYEGSILQLFIK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:119397; OMIM:154550
A;Map position: 15q22-15qter
C;Superfamily: yeart mannose-6-phosphate isomerase
C;Seywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                         87
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                                                                                                                                                                                                                         58 D----AKAAMTELKSCIDGLQPMH----KAELVKLLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 70.5; Di
25:7%; Pred. No. 13;
tive 19; Mismatches
         ed. No. 11;
Mismatches
            Pred.
                                                                                                   18 CRMATG---EDNDEFFMDFLQTLLVG
         Local Similarity 23.5%; Pr
nes 23; Conservative 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.0%
Best Local Similarity 25:7%
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-423 <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S41122
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            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene:
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A;Molecule type: DNA
A;Rosidues: 1-609 <MUR>
A;Cross-references: EMBL:AL109739; NID:e1534774; PIDN:CAB52270.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h-; cosmid c343
                                                                                                                                                                                                                                                         <MAT>
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C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T38656
R; Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1997
A; Reference number: 221804
A; Reference number: 221804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
S54143
SRP 54 protein - human (fragment)
SCSP 54 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Spate: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S54143
B;Reference number: S54143
A;Reference number: S54143
A;Accession: S54143
R; Bernstein, H.

submitted to the EMBL Data Library, November 1989
A; Reference number: $14553
A; Accession: $144553
A; Molecule type: mRNA
A; Residues: 142, DV, 45-504 <BBR2>
A; Cross-references: EMBL:X16319; NID:954193; PIDN:CAA34386.1; PID:954194
C; Superfamily: signal recognition particle 54K protein
F; 2-504/Product: signal recognition particle 54K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA_A;Residues: 1-504 <PAT>A;Residues: 1-504 <PAT>A;Cross-references: EMBL:X86373; NID:g784998; PIDN:CAA60132.1; PID:g784999 C;Superfamily: signal recognition particle 54K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 KGGGALSAVAATKSPIIFIGTGEHIDDFEPFKTQPFISKLLGMGDIEGLID-----KVN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KGSRALLLVALTLECICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
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                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 ELKLDDNEALIEKLKHGQFTLRDMYEQFQNIMKMGPFSQILGMIPGFGTDF 359
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Length 504;

40; Indels

14.1%; Score 76.5; DB 2; 32.4%; Pred. No. 3.7; Live 16; Mismatches 40;

Best Local Similarity 32.49 Matches 36; Conservative

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Query Match

A; Status: preliminary

57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99

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12.8%; Score 69.5;
                                                          Query Match
                                                        DB 2; Length 609;
                                                      13.5%; Score 73;
A; Map position: 1
A; Introns: 44/1; 96/2; 325/3
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A; Gene: SPDB:SPAC343.07

C;Genetics:

Query Match

us-09-768-826-47.rpr

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Ribolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
Aritle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
Areference number: A86625; MUID:21235186; PMID:11337471
Arecession: G86790*
Arecession: G86790*
Arecelle type: DNA
Aresidues: 1-540 <STO>
Arecelle type: DNA
Arecelle type: CSTO>
Arecelle type: CSTO>
Arecelle type: DNA
Arecelle type: DNA
Arecelle type: CSTO>
Arecelle type: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibronectin-binding protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86790
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                                                                              3,
                                                                                                                                                                                                                                                               2239 QLLHLTQSEQELEQDA-AARTAMQG--SGLQPLQRSQIVQAIARVLGGGGGCG 2288
                                                                                                                                                                          44 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.7%; Score 69; DB 2; Length 540; Best Local Similarity 30.6%; Pred. No. 25; Matches 22; Conservative 9; Mismatches 37; Indels
Best Local Similarity .32.1%; Pred. No. 1.2e+02;
Matches 17; Conservative 14; Mismatches 19; Indels
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354 KLKQAVKFLGEQ 365
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                                                              April 28, 2003, 14:39:06 ; Search time 16.9588 Seconds (without alignments) 182.172 Million cell updates/sec
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                                                                                                                       542
1 MKGSRALLLVALTLFCICRM.....VQVLGSQDGAGTDYKDDDDK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6,
Sequence 8,
Sequence 8,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-864-357F-1
US-08-864-357F-2
US-08-821-451A-2
US-09-263-810-2
                                                                                                                                                                                                                of hits satisfying chosen parameters:
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US-08-933-149-8
US-09-082-343-8
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US-08-864-357F-4
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US-09-215-818-6
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US-08-569-853-2
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                                                                                                                                                                                           262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                            US-09-768-826-47
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Match Length
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9
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79.5
74.5
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71
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Maximum DB
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Sequence 2, Appli	US-08-242-677-2	Н	1621	11.7	63.5	45
Sequence 43, Appl	US-08-149-223A-43	m	745	11.7	63.5	44
Sequence 43, Appl	US-08-458-731-43	m	745	11.7	63.5	43
Sequence 43, Appl	US-08-480-150A-43	7	745	11.7	63.5	42
Sequence 43, Appl	US-08-484-596A-43	7	745	11.7	63.5	41.
Sequence 43, Appl	US-08-484-158B-43	7	745	11.7	63.5	.40
Seguence 5, Appli	US-08-862-903-5	7	745	11.7	63.5	39
Sequence 43, Appl	US-08-484-993B-43	7	745	11.7	63.5	38
Sequence 5, Appli	US-08-453-952-5	-	745	11.7	63.5	37
Sequence 9, Appli	US-08-038-948-9	Н	745	11.7	63.5	36
Sequence 5, Appli	US-08-453-472-5	-	745	11.7	63.5	32
Sequence 2, Appli	US-08-559-896B-2	4	652	12.0	65	34
Seguence 4, Appli	US-08-559-896B-4	4	139	12.0	65	33
Seguence 22, Appl	US-09-046-158A-22	4	1139	12.2	99	32
Sequence 23, Appl	US-08-912-276-23	4	69	12.2	99	31
Seguence 11, Appl	US-08-653-648A-11	4	909	12.3	66.5	30
Seguence 3, Appli	US-08-891-298-3	4	909	12.3	66.5	29
sednence I, Appli	US-08-987-439-I	า	2233	12.5	68	28

#### ALIGNMENTS

.; 0 APPLICANT: Xing, Ruye
TITLE OF INVENTION: HIGHLY PURIFIED CYTOKINE ACTIVATING FACTOR AND METHODS
TITLE OF INVENTION: OF USE
TITLE OF INVENTION: OF USE
TITLE OF INVENTION: OF USE
CURRENT APPLICATION NUMBER: US/09/620,093A
CURRENT FILING DATE: 2000-07-23
PRIOR PILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: 60/197,619
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOY: 2.1 Gaps Length 70; Score 142; DB 4; Length 70 Pred. No. 1.2e-10; 7; Mismatches 24; Indels ; LOCATION: (63) ; OTHER INFORMATION: Xaa = any residue US-09-620-093A-6 Sequence 6, Application US/09620093A Patent No. 6420337 26.28; 49.28; any Iyer, Subramanian APPLICANT: Nguyen, Tay N. APPLICANT: Wu, Dauh-Rurng n gallus Xaa Ouery Match Best Local Similarity Matches 30; Conserv LOCATION: (54) OTHER INFORMATION: GENERAL INFORMATION: TYPE: PRT ORGANISM: Gallus NAME/KEY: UNSURE NAME/KEY: UNSURE US-09-620-093A-6 70 APPLICANT: APPLICANT: SEQ ID NO 6 LENGIH: RESULT 1

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87 **EFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQ** 9 28 ŏ a

v 88 99 I 88 99 ò q

US-08-455-896-8; Sequence 8, Application US/08455896; Patent No. 5668267

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16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09082343
Patent No. 5968754
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLENIG, TIMOTHY P.
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,343
    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 2;
Pred. No. 0.00033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                    6029-6040
                                          APPLICATION NUMBER: US/08/933,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/455,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HENDERSON, MELODIE W.
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 95:
                                                                                                                                                                REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEO ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
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27.8%;
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TELEFAX: (314) 727-6092
INFORMATION FOR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         LENGTH: 91 amino acids
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                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 27; Conserv
                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63105-1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-933-149-8
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                 APPLICANT: WATSON, MARK A.
APPLICANT: ELEMING, THOOTHY P.
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ROGERS, HOWELL & HAFERKAMP
STREET: ST733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAMMAGLOBIN, A SECRETED MAMMARY SPECIFIC BREAST CANCER PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Indels
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 92; DB 1;
27.8%; Pred. No. 0.00033;
Live 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESSONDENCE ADDRESS:
ADDRESSEE: HAFERRAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9527
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08933149
Patent No. 5922836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: MAMMAGLOBIL
TITLE OF INVENTION: MAMMARY SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.8%
Matches 27; Conservative
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linear
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
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STATE: MAL.
COUNTRY: USA
7 63105-1817
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: MISSOURI
                                                                                                                                                                                                                                             63105-1817
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US96/08235 FILING DATE:
                                                                                                                                              PCT-0596-08235-8; Sequence 8, Application PC/TUS9608235; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-821-451A-4
; Sequence 4, Application US/08821451A
; Patent No. 6066724
; GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; Sco
27.8%; Pre
tive 18;
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (314) 727-5188 (318) TOT-6092 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.07
Best Local Similarity 27.85
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
NO
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TITLE OF INVENTION: B1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                      ST. LOUIS
MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-08235-8
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                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                       Dp
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                                                                                                                                                                                                                                                    1 MKLAVTLTLVTLALCCSSASAEIC------PSFQRVIETLLMDTPSS-YEAAMELFS 50
                                                                                                                                                                                                                 1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TINOTHY P.
TITLE OF INVENTION: DAMASRY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSEE: ROCERS, HOWELL & HAFERKAMP
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 92; DB 3; Length 91; 27.8%; Pred. No. 0.00033; Live 18; Mismatches 36; Indels
                                                                                                                                            17.0%; Score 92; DB 2; Length 91; 27.8%; Pred. No. 0.00033;
                                                                                                                                                                                36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,253
                                                                                                                                                                                                                                                                                          55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS 91
                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952726
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APPLICATION NUMBER: 08/455,896
FILLING DATE: 05/31/1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09082253 Patent No. 6004756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                               Best Local Similarity 27.89
Matches 27; Conservative
91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.0
Best Local Similarity 27.8
Matches 27; Conservative
                                SS: single
linear
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                                                                         protein
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ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
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                 TYPE: amino acid
STRANDEDNESS: si
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STATE: MISSOURI
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                                                 TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: N
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                                                                                                       US-09-082-343-8
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US-09-082-253-8
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                                                                                                                                              Query Match
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16; Gaps
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                                                                                                                                                                                                                                   APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: DAS SEQUENCE AND ENCODED
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 5; he.,
, 0.00033;
, 36; Indels
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VENTION: Human Endometrial Specific Steroid-
VENTION: Binding Factor I, II and III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                         51 PDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIAQS 87
                                                                                                                                                                                                                                                                                                                                                                                                  E: ROGERS, HOWELL & HAFERKAMP 7733 FORSYTH BOULEVARD, SUITE 1400
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Indels 16; Gaps
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APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: FEAGEWIS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
                                                                                                                                                                                                                                                                                                                                                                                          Length 90;
                 APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNY CAGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 33,2800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHAX: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                            ; Score 91; DB 4;
; Pred. No. 0.00043;
16; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastsEO for Windows Version 2.0
SUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Billing-Medel, Patricia A.
Cohen, Maurice
Colpitts, Tracey L.
Friedman, Paula N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-912-276-15
; Sequence 15, Application US/08912276
; Patent No. 6183952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon, Julian
Granados, Edward N.
Hodges, Steven C.
Klass, Michael R.·
Kratochvil, Jon D.
                                                                                                                                                                                                                                                                                                                                                                                            16.8%;
29.5%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKATLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECKEr, Cheryl L
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.5%
Matches 28; Conservative
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-263-810-4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.8%; Score 91; DB 3; Length 90; 29.5%; Pred. No. 0.00043; Live 16; Mismatches 35; Indels
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GENERAL INFORMATION:

APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz

TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

CITY: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                   325800-521 (PF257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 APPEAVAKLGVKRCTDQMSLQKRSLIAEVLVKIL 85
                                                                                                                                                                                               SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,451A
FILING DATE: March 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,724
FILING DATE: March 21, 1996
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,810
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09263810 Patent No. 6174992
                                                                                                                                                                                                                                                                                                                                                                                        NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32FELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 29.59
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
      STREET: 6 DLC.
CITY: ROSELAND
THATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
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Sequence 3, Application US/08864357F
Patent No. 6255281
GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflamm
FITTLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
                                                                                                                                16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKGSRALLLVALTLFC-----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                              1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                    Indels
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  Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR TITLE OF INVENTION: DIFFECTING DISEASES OF THE BREAST FILE REFERENCE: 5972 US.P.2
CURRENT APPLICATION NUMBER: US/09/215,818A
CURRENT FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.8%; Score 91; DB 4;
29.5%; Pred. No. 0.00043;
Live 16; Mismatches 35
  ; Score 91; DB 4;
; Pred. No. 0.00043;
16; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                          :| || :| || :| || 51 APPEAVAAKLGVKRCTDQMSLQKRSLIAEVLVKIL 85
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                                                                                                                                                                                            55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APELICATION NUMBER: 08/912,276
EARLIER FILING DATE: 1997-08-17
EARLIER FILING DATE: 1997-08-17
EARLIER FILING DATE: 1996-08-19
EARLIER FILING DATE: 1996-08-19
EARLIER FILING DATE: 1997-08-15
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
SERICH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
                                                                                                                                                                                                                                                                                                                                    US-09-215-818-6
; Sequence 6, Application US/09215818A
; Patent No. 6379671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.8%
Best Local Similarity 29.5%
Matches 28; Conservative
Query Match
Best Local Similarity 29.58
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Colpitts, Tracey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-215-818-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ
SOFTWARE: Pa
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LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 90; 0.00043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
MAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/FOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART 6 OLSTEIN STREETS 6 BECKER FARM ROAD CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : | | | : : : : : | | : | | : | | SI APPEAVAAKLGVKRCTDQMSLQKRSLIAEVLVKIL 85
                                                                                                                                                                                                                                                                                                                                                        Query Match

16.8%; Score 91; DB
Best Local Similarity 29.5%; Pred. No. 0.00
Matches 28; Conservative 16; Mismatches
                      REFERENCE/DOCKET NUMBER: 5972.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS.
OPERATING SYSTEM: MS-DOS.
CURRENT APPLICATION DERFECT 5.1
APPLICATION NUMBER: · US/09/583,169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/821,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09583169
Patent No. 6338948
                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: No. 6183952e
                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201-994-1744
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  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07068
                                                                                                                                                                                                                                                                                                            US-08-912-276-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-583-169-4
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DB 4; Length 75;

15.8%; Score 85.5;

Query Match

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Jian Ni, Guo-Liang Yu and Reiner Gentz
VENTION: Human Endometrial Specific Steroid-
VENTION: Binding Factor I, II and III
                                                                                                                                                                                                                                                                                                ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM, MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,451A
FILING DATE: MARCH 21, 1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 60/014,724
FILING DATE: MARCH 21, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                           Sequence 2, Application US/08821451A; Patent No. 6066724
GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu
                                                                                                                                                                                                          TITLE OF INVENTION: HUT
TITLE OF INVENTION: B1:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/
OPERATING SYSTEM:
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Matches 25; Conserv
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APPLICANT: Claragen, Inc. & NIH
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatc
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT APPLICATION NUMBER: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Claragen, Inc. & NIH
TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammatc
TITLE OF INVENTION: Fibrotic Conditions
FILE REFERENCE: 116142/2
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                                                                                 30 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                         6 FAHVIENLLIGTPSS-YETSLKEFEPDDTMKDAGMQMKKVLDSLPQTTRENIMKLTEKIV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 74.5; DB 4; Length 69; 27.4%; Pred. No. 0.035; Live 17; Mismatches 27; Indels
Pred. No. 0.0016;
                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/864,357F
CURRENT FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                  : Sequence 1, Application US/08864357F; Patent No. 6255281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08864357F Patent No. 6255281
                 Best Local Similarity 35.5%;
Matches 22; Conservative 1
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: human
US-08-864-357F-1
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US-08-864-35,7F-2
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LENGTH: 70
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LENGTH: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNL----
NAME: MULLINS, J.G.
RECISTRATION NUMBER: 33,073
REFERNCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMINICATION INFORMATION:
TELECOMMINICATION: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 PPPEALAAKLEVKHCTDQISFKKRLSLEKVLVEIV 85
                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 71; DB
ilarity 26.3%; Pred. No. 0.14
Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 28, 2003, 14:45:28 Job time: 18.9588 secs
                                                                                                                                                                                                         90 AMINO ACIDS
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                           201-994-1744
                                                                                                                                                                                                                                                                                 TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
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O85808 borrelia bu P94238 borrelia bu Q44978 borrelia bu Q95jy6 macaca fasc

Q8ryj9 oryza sativ

Q8qx12 sorghum mos Q8qx11 sorghum mos O57942 pyrococcus

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Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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EDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 362; DB 4; Length 95;
Pred. No. 1.4e-33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bingle C.D.;
"Human RYD5, a new secretoglobin.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY026938; AAK08972.1; -
SEQUENCE 95 AA; 10457 WW; F629AF06C96D2392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                            95 AA
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                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
Putative ligand binding protein RYD5
                                                                                     09VABB
09UTB3
09UTB3
035651
09P779
09PPS1
09PRN0
09FRN0
09SYB9
09SYB9
09SYB9
09SYB9
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09SYB9
09SYB9
                                    Q95JY6
Q8QXL2
Q8QXL1
Q57942
Q9XSW4
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Q931R6
Q01837
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                  P94238
Q44978
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Matches 71; Conservative
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                                      742
3071
3071
362
454
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609
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1087
1719
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NCBI_TaxID=9606;
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Q05702;
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O51827 pseudomonas
Q9cfy4 lactococcus
P87112 schizosacch
O95247 homo sapien
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Oglvg2 arabidopsis
Ol3450 saccharomyc
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Q8ycg5 brucella me
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homo sapien
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                                                                            (without alignments)
832.774 Million cell updates/sec
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                                                                 April 28, 2003, 14:36:31; Search time 20.2887 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                          EDNDEFFMDFLQTLLVGTPE.....VQVLGSQDGAGTDYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8xm24
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        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                               Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                            671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                       US-09-768-826-47_COPY_24_105
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Maximum Match 100%
Listing first 45 summaries
                                               protein search, using sw model
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Q8VD96
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_organelle:*
sp_phage:*
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sp_bacteria:*
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Matches 27; Conserv
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SEQUENCE 2104 AA
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PubMed=11792842
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10117;
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STRAIN-FISCHER; ITSUB-OLFACTORY EPITHBLIUM;
MEDLINE-92007724; PubMed-1915264;
Dear T.N., Boehm T., Keverne E.B., Rabbitts T.H.;
"Novel genes for potential ligand-binding proteins in subregions of the olfactory mucosa.";
the olfactory mucosa.";
LEMBO J. 10:2813-2819(1991).
EMBL. X60661; CAA43068-1;
InterPro: IPR000329; Uteroglobin.
SMART: SM00096; UTG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular evolution of the Metazoan protein kinase C multigene
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMR-2002 (TrEMBLrel. 07, Last sequence update)
Stress-responsive protein kinase (PRKSD).
Suberites domuncula (Sponge).
Eukaryota: Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Hadromerida; Suberitidae; Suberites.
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Kruse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
Mueller W.E.G.;
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transeferase.
SEQUENCE 478 AA; 54098 WW; 6B38FF5FD88D6332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 AA; 10401 MW; 25A4BBBB4977E247 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Potential ligand-binding protein.
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Pred. No. 2.1e-25;
9; Mismatches 5;
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InterPro; IPR002290; Ser_thr_pkinase.
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ProDom; PD000001; Euk_pkinase; I.
SMART; SM00220; S_TKC; I.
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EMBL: Y13101; CAA73555.1; -.
HSSP; P24941; 1HCL.
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80.0%;
                                                                                                                         Rattus rattus (Black rat)
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Matches 56; Conservative
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Best Local Similarity
Matches 26; Conserv
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721 KDSDAFLYDFADILKQLLANSAQEYYEVMCNAYNNGNGEKFKFVSGKF-----LE 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria: Firmicutes; Bacillus/Clostridium.group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBL_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%; Score 76; DB 16; Length 2104;
llarity 29.0%; Pred. No. 22;
Conservative 10; Mismatches 34; Indels 2:
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable alpha-N-acetylglucosaminidase.
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CC10 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003188; BAB80572.1; -
InterPro; IPR002048; BF-hand.
InterPro; IPR000421; FA58_C.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                    PRT; 2104 AA
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                                                                                               ||:: :::| ::|:|:||:||ELIQDAMRILEEEEGSGSDEEDDND 311
                                                                  57 ELVKLLVQVLGSQDGAGTDYKDDDD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00754; F5_F8_type_C; 1.
Pfam; PF00041; fn3; 1.
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Gutlerrez-Sagal R., Nieto A.;
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium perfringens.
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STRAIN-13 / TYPE A;
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SEQUENCE FROM N.A.
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Length 2458;

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Query Match
Best Local Similarity
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P87112;
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                                      Matches
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Q9CFY4
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                                                                                                                                                                                                                                                                                                                                                                   27 FFQVLEFLFMGS-ESSYEAALKFYNPGSDLQDSGTQLKKLVDTLPQKTRMNIMKLSEIIL 85
'Cloning and sequencing of a cDNA encoding hamster uteroglobin/clara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nowak-Thompson B., Chaney N., Wing J.S., Gould S.J., Loper J.E.; "Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas fluorescens Pf-5.";
                                                                                                                                                                                                                                                                                                           5,
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Pseudomonas.
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"Identification and sequence analysis of the genes encoding a polyketide synthase required for pyoluteorin biosynthesis in Pseudomonas fluorescens Pf-5.";
Gene 204:17-24(1997).
                                                                                                                                                                                                                                                             5; DB 11; Length 96;
0.68;
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              cell 10 kDa protein.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 137041; AAL13149.1;
InterPro; IPR003628; Uteroglabi.
InterPro; IPR000329; Uteroglabin.
Pfam; PF01099; Uteroglabin; 1.
Probom; PD012475; Uteroglabin. 1.
                                                                                                                                                                                                              POTENTIAL.
5EB9CBDD46143389 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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R InterPro; IPR001294; Ketoacyl-synt.
InterPro; IPR0003880; Ppantne_attach.
R InterPro; IPR00013880; Ppantne_attach.
R InterPro; IPR001385; Thiolase.
R Pfam; PF00698; Acyl_transf; 1.
R Pfam; PF02010; Ketoacyl-synt; 2.
R Pfam; PF02001; Ketoacyl-synt. 2.
R PF0217E; PS00006; B_KETOACYL_SYNTHASE; 2.
R PROSITE; PS00006; B_KETOACYL_SYNTHASE; 2.
R PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN_1.
R PROSITE; PS000098; THIOLASE_I; UNKNOWN_1.
R PROSITE; PS000098; THIOLASE_I R PROSITE; PS0000098; THIOLASE_I R PROSITE; PS0000098; THIOLASE_I R PROSITE; PS0000098; THIOLASE_I R PS0000098
                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                        PROSITE; PS00404; UTEROGLOBIN_2; UNKNOWN_1
                                                                                                                                                                                                                                                                     17.4%; Score 74.5; 32.4%; Pred. No. 0.
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EMBL; AF081920; AAC38075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99194726; Pubmed-10094695;
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                                                                                                                                                                                                              1 18
96 AA; 10509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyketide synthase type I.
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas fluorescens
                                                                                                                                                      SM00096; UTG; 1
                                                                                                                                                                                                                                                                                       Local Similarity
ses 22; Conserv
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86 TSPLCNQD 93
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051827
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sp. lactis IL1403.";
Genome Res. 11:731-753(2001).

EMBL; AE006365; AAK05425.1; -.
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMLARITY: TO YEAST NOT1.
EMBL; 295334; CAB08600.1; --
Hypothetical protein; Nuclear protein; Transcription regulation.
SEQUENCE 2100 AA; 237132 MW; 760ADA97C406EICC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Lactococcus.
                                                                                                                                   2239 QLLHLTQSEQELEQDA-AARTAMQG--SGLQPLQRSQIVQAIARVLGGGGCG 2288
                                                     .;
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                                                                                                   21 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 540; 25;
                                                     19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 AA; 61285 MW; 4DAC3CCCBCF72867 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
variable of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
16.3%; Score 69.5; DB 2; 32.1%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                      AA.
                                                  14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 69; 30.6%; Pred. No.
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06, Last sequ
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                                                                                                                                                                                                                                                                                      PRT;
                                                  17; Conservative
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Best Local Similarity
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MEDLINE=99077764; PubMed=9858827;
Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
"Identification of the WBSCR9 gene, encoding a novel transcriptional regulator, in the W111ana-Beuren syndrome deletion at 7q11.23.";
Cytogenet. Cell Genet. 87:238-246(1998).
EMBL: AF084479; AAD08675.1;
InterPro; IPR001487; Bromodomain.
InterPro; IPR001405; DT_dom.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 68; DB 4; Length 1483; 23.7%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                         PRINTS; PRO0503; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 1.
SMART; SM00184; RIG; 1.
PROSITE; PSS0014; BROMODOMAIN_2; 1.
SEQUENCE 1483 AA; 170903 MW; A47E0365439C5EC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bromodomain adjacent to zinc finger domain 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones M.H., Hamana N., Nezu J., Shimane M.;
"A novel family of bromodomain genes.";
Genomics 63:40-45(2000).
EMBL, AB032253; BAA68210.1; --
HSSP, Q92831; 1B91.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00628; PHD; 1.
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                                                                                                                                                                                                                                                        Pfam; PF00439; bromodomain; 1.
Pfam; PF00628; PHD; 1.
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                       SEQUENCE FROM N.A.
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Q9UIGO;
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                                                                         10 FLQTLLVGTPEELYEGTLGKYNVNEDAK -- AAMTELKSCIDGLQPMHKAELVKLLVQVLG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"A novel human gene, WSTF, is deleted in Williams Syndrome.";
Genomics 54.241-249(1998).
EMBL; ARC72810; AAC97879.1; -.
HSSP; Q92831; 1891.
TRANSFAC; T04145; -.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001487; DTT dom.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001841; Znf_PHD.
16.0%; Score 68.5; DB 3; Length 2100; 33.3%; Pred. No. 1.6e+02; Live 12; Mismatches 25; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%; Score 68; DB 4; Length 1425; 23.7%; Pred. No. 1.1e+02; tive 20; Mismatches 34; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50014; BROMODOMAIN_2; 2.
1425 AA; 164226 MW; 20428BC35F4FB72F CRC64;
                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transcription factor WSTF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AELVKLLVQ------VLGSQDGAGTDYKDDDDK 82
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MEDLINE-99047530; PubMed-9828126;
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Pfam; PF00628; PHD; 1.
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SMART; SMO0297; BROMO; 1.
SMART; SMO0249; PHD; 1.
SMART; SMO0184; RING; 1.
                 Best Local Similarity 33.38 Matches 21; Conservative
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                                                                                                                                                                                            1922 SQD 1924
                                                                                                                                                      68 SQD 70
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   Query Match
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095277
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095247
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                                                                                                                                                              15.9%; Score 68; DB 4; Length 1527; 23.7%; Pred. No. 1.2e+02; ive 20; Mismatches 34; Indels
PRINTS; PRODSO; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 1.
SMART; SM0149; PHD; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
SEQUENCE 1527 AA; 176033 MW; DIICA368CD55EFIC CRC64;
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SGD; S0005215; BNI1
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=X2180;
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                                       1046 DGNOELLNFLRSDLIEVATRLQKGGLGYVEETSEFEARVISLEKLKDFGECVIALQ---- 1101
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Dong J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologis A.;
"Full Length CDNA of gene At5g60120 (GI:15238620).";
Submitted (JAN-2002) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
DNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELK-----SCIDGLQPMHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to tyrosine aminotransferase (Hypothetical 50.6 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                1102 ASVIKKFLOGFMAPKOKRRKLOSEDSAKTEEVDEEKK 1138
                                                                                    56 AELVKLLVQ------VLGSQDGAGTDYKDDDDK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s; Score 67.5; D
s; Pred. No. 19;
10; Mismatches
                                                                                                                                                                                                                                            317
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PFG0847; AP2-Gomain; 1.
SMART; SMO0380; AP2; 1.
SEQUENCE 317 AA; 35036 MW;
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Best Local Similarity 28:8'
Matches 15; Conservative
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                                                                                                                                                                                                                                            PRELIMINARY;
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01-MAR-2002
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C08VXX7
TD 01-MA
DT 01-MA
DT 01-MA
DT 01-JU
DE PULET
DE PULET
COC SELNET
COC S
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Q8QZR1
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Suromids II; Brassicales; Brassicaee; Arabidopsis.
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequer features of the regions of 3,076,755 bp covered by sixty Pl and TAC clones.";
DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA:
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                             327 LKSILQRTPQEFYQDTLSFLKSNADLCYGAL---SAIPGLQPVRPSGAMYLMVGI 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                   11 LQTLLVGTPEELYEGTLGKYNVNED-AKAAMTELKSCIDGLQPMHKAELVKLLVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 485;
                                                                                                                                                           Length 454;
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                                                                                                                                                                                                                     Indels
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; D38411; BAA22512.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB019231, BAA96941.1; -.
InterPro: IPR001471; TF ERF.
Pfam; PF00847; AP2-domain; 1.
SMART; SMO8380; AP2; 1.
SEQUENCE 485 AA; 53164 MW; BEFB290E407FC3D5 CRC64;
EMBL; BC024264; AAH24264.1; -.
EMBL; BC025934; AAH35934.1; -.
Hypothetical protein; Aminotransferase; Transferase.
SEQUENCE 454 AA; 50565 WW; CDB6E1E6CDB5DC7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
AP2 domain transcription factor-like.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                           DB 11;
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                                                                                                                                                        Query Match 15.8%; Score 67.5; DF Best Local Similarity 33.9%; Pred. No. 30; Matches 19; Conservative 11; Mismatches
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28.8%; Pred. No. 33;
tive 10; Mismatches
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Search completed: April 28, 2003, 14:43:29 Job time : 23.2887 secs

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(without alignments)
278.964 Million cell updates/sec
                                                                                                                                                                April 28, 2003, 14:33:15; Search time 39.1684 Seconds
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp·embl/AA1983.
/SIDS2/gcgdata/geneseq/geneseqp·embl/AA1984.
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl
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Listing first 45 summaries
                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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08
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

SUMMAKIES			Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Human albumin fusi						778 Lymphocytoma proli		1
SOM			ΙD	AAB70079	ABG65513	AA021685	AAB723	AAW878	AAB32]	AAW26	AAR55778	AAW116	AAW87569
			DB	22	23	23	22	20	21	18	15	18	20
			Match Length DB	: ``	105	95	70	75	75	96	70	70	20
	æ	Query	Match	100.0	100.0	84.8	33.3	30.05	20.0	19.0	18.6	18.6	18.6
			Score	427	427	362	142	85.5	85.5	81	79.5	79.5	79.5
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WPI; 2001-244245/25

Human uteroglobin.	Human Clara cell p	OMTKY3 ch	hPSTI.SSImutant ch	Bovine mammary tis	_	ப	Rabbit uteroglobin	Murine mature chor	Murine chordin (CH	Mouse uteroglobin-	ne uteroc	Lung cancer associ	ce hum	Ad5 fiber knob dom	Lactococcus lactis	Human BA21-beta pr		Protein rCD44HS.	Human polypeptide	. Human polypeptide	Borna disease viru	Human JAK2 protein	Drosophila melanog	Plasmodium falcipa	Murine mature chor	Murine chordin-lik	Plasmodium falcipa	Herbicidally activ	Human ORF1596 prot	Modified human/mou	Flag epitope tag f	hylococc	phylococc	. Staphylococcus aur	
AAB32128	AAB64165	AAW26363	AAW26364	AAB87666	ABG20226	AAW87857	AAB32129	AAE03735	AAE03734	AAW87859	AAB32131	AAB58143	AAE23794	AAW77363	ABB54664	AAW81172	AAW81173	AAM48312	AAM39384	AAM41170	AAY79286	AAW76425	ABB58776	AAW18011	AAE03733	AAE03732	AAW18010	ABB91422	ABP32623	ABB08237	9	AAU34143	AAU37017	AAU37403	
21	22	18	18	22	22	20	21	22	22	20	21	21	23	19	23	19	19	23	22	22	21	19	22	18	22	22	18	23	23	23	. 22	22	22	22	
20	91	78	78	102	452	69	69	936	962	75	75	119	187	47	540	1527	53	167	423	465	95	1139	457	139	323	345	652	842	92	1594	24	8	5795	28	
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79.5	σ	9	9	9	9	4		73	73	σ	69.5	σ	σ	69	69	68	89	29	29	29	99		65.5	65	65	65	65	65	64.5	4	64	64	64	64	
11	12	13	14	15	16	17	18	19	20	21	22	23	24	~	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	. 41	42	43	44	4.5	

### ALIGNMENTS

dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotectant; noortropic; anticonvulsant; vaccine; antialzheimers; antiperkinsonian; antimicrobial; vulnerary; gene therapy; immune disorder; hyperproliferative; cardiovascular; angiogenic; neurological; infection. Human; secreted protein; immunomodulatory; antisclerotic; Ruben SM; Soppet DR, AAB70079 standard; Protein; 105 AA (HUMA-) HUMAN GENOME SCI INC. 15-AUG-2000; 2000WO-US22350. Ebner R, Human secreted protein #18 (first entry) Shi Y, Young PE, WO200112776-A2. Homo sapiens 16-AUG-1999; 14-MAY-2001 22-FEB-2001 AAB70079; AAB70079 

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The present sequence is one of 18 novel human secreted proteins. The nucleic acids encoding the proteins and the proteins themselves may be used in the prevention, dagnosis and treatment of diseases including immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases. (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), anglogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences. In samples. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of protein expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 EDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDARAAMTELKSCIDGLQPMHKAELVK 83
                                   Nucleic acids encoding 18 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antinferulity; antinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 427; DB 22;
100.0%; Pred. No. 5.7e-45;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human albumin fusion protein #2188.
                                                                                                              Claim 11; Page 373; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG65513 standard; Protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVQVLGSQDGAGTDYKDDDDK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLVQVLGSQDGAGTDYKDDDDK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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2000US-199384P.
2000US-256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic; antlarthritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
N-PSDB; AAF76860.
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Synthetic.
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25-APR-2000;
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Matches
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The present invention relates to albumin (HA, also known as human serum therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin certains the shelf-life of protein X, and may increase its blological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disorders (e.g. acquired immunodeficiency syndrome, AlbS), endocrine disorders (e.g. acquired immunodeficiency syndrome, AlbS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzhehmer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, maninglis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABGG5518 represent albumin fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiarterlosclerotic; cytostatic; HIV; antiallergic; antianaemic; antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonian; cerebroprotective; anti.Inflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; anteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia; Parkinson's disease; epilepsy; stroke; knockin humanised animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 EDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVK 83
                                                                                             New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 427; DB 23;
100.0%; Pred. No. 5.7e-45;
Live 0; Mismatches 0;
                                                                                                                                                        Claim 1; Page 2082; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein SEQ ID No 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO21685 standard; Protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLVQVLGSQDGAGTDYKDDDDK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic animal; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LLVQVLGSQDGAGTDYKDDDDK 82
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2000US-248642P.
2000US-249824P.
2000US-252824P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0
Best Local Similarity 100.0
Matches 82; Conservative
                  Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AA;
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16-NOV-2000;
21-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000;
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                  Rosen CA,
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                     19-JUL-2000; 2000WO-US19643.
                                                        23-JUL-1999; 99US-0145317.
14-APR-2000; 2000US-0197619.
                                                                                                                                                     Wu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V12-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.3
Best Local Similarity 49.2
Matches 30; Conservative
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                                                                                                                                                    Nguyen TN,
                                                                                                                                                                                     WPI; 2001-123262/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AA;
                                                                                                                (DCAD-) DCA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder, AIDS, allergies, anaeania, asthma; cardiovascular disease e.g. congestive heart failure, ischaemic heart disease; developmental disorder e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g. Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke. The SECP polynucleotide and polypeptide are further useful for analysing the proteome of a tissue or a cell type. The polynucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, and for somatic or germline gene therapy, and further for generating hybridisation probes useful in mapping the naturally occurring genomic sequence. This sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated human secreted protein (SECP) polypeptide from 63 fully defined protein sequences given in the specification. The polypeptide is useful for the diagnosing/treating of a disease with decreased/overexpression of SECP. Examples of disorders associated with abnormal expression of SECP include a cell proliferative disorder e.g. arterlosclerosis, cancers; autoimmune/inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine activating factor; CAF; tumour necrosis factor alpha; TNF-alpha; interleukin-1beta; IL-1beta; transforming growth factor beta; TGF-beta; immune response; cancer; sepsis; septic shock; bacterial infection;
                                                                                 ILA M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burford N;
Hafalia AJA, Tang YT, Bandman O, Warren BA, Honchell CD;
Thangavelu K, Lee S, Xu Y, Yang J, Lal PG, Tran B;
Duggan BM, Sapperstein SK;
                                                                                                                                                                                                                                                               Human secreted proteins and polynucleotides for diagnosing, treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                preventing disorders of cell proliferative, cardiovascular, developmental, neurological and autoimmune/inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.8%; Score 362; DB 23; Length 95; Best Local Similarity 98.6%; Pred. No. 5.5e-37; Matches 71; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine activating factor CAFb amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 168; 229pp; English.
08-DEC-2000; 2000US-254305P.
18-DEC-2000; 2000US-256448P.
                                                      (INCY-) INCYTE GENOMICS INC
                                                                               Yao MG, Gancon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                             Sanjanwala M,
Ding L, Hafal
Lu DAM, Thang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2001
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ð Dp ö qq RESULT 4 AAB72211

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This invention relates to a cytokine activating factor (CAF) protein which upregulates the expression of tumour necrosis factor alpha which upregulates the expression of tumour necrosis factor alpha (TNF-alpha), interleukin-lbeta (IL-lbeta) or downregulates expression of transforming growth factor beta (TGF-beta). A composition, preferably a food product, containing a CAF protein is useful for regulating an immune response and treating cancer in an animal. It is also useful for treating or preventing sepsis and/or septic shock and bacterial infection in an animal. The present sequence represents the full length CAFb protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crohn's disease; ulcerative colitis; pancreatitis; peritonitis; allergy; multiple organ failure; adult respiratory distress syndrome; acute renal failure; organ transplant rejection; autoimmune uveitis; corneal transplant surgery; neonatal RDS; cytomegalovirus retinitis; pneumonia; cystitis; schistosomiasis; vaginal candidiasis; fibrosis; neonatal broncho-pulmonary dysplasia; haemodialysis; glomerulopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uteroglobin; phospholipase A2; fibronectin; inflammation; asthma; cystic fibrosis; premature labour; infertility; rheumatoid arthritis; type I diabetes; nephropathy; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cytokine activating factor, useful for regulating an immune response and treating cancer and sepsis in an animal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 142; DB 22; Length 70;
49.2%; Pred. No. 6.2e-10;
tive 7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW87858 standard; protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat uteroglobin-like protein CC10.
                                                                                                                                                   Claim 1; Page 61; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0864357
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pulmonary inflammation -
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/label=
                 Zheng F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Homo saplens;
                                                WPI; 2000-687100/67
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                    75 AA;
                 Mukherjee AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Sim
Matches .22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW26362;
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
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AAW26362
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                                                                                                                                                                                                             The present sequence represents a uteroglobin-like protein. Recombinant human uteroglobin inhibits phospholipase A2 (PLA2), and binds to fibronectin. Inhibition of PLA2 is used to treat or prevent a wide range of systemic and ocular inflammations, asthma, cystic fibrosis, premature labour, infertility, rheumations asthma, cystic fibrosis, premature inflammatory bowel disease, Crohn's disease, ulcerative colitis, pancreatitis, peritonitis, allergy, multiple organ failure, adult respiratory distress syndrome (RDS), acute renal failure, inflammation secondary to infection or surgery, and organ transplant rejection. Some specified applications are in autoimmune uveitis, corneal transplant surgery, neonatal and adult RDS, cytomegalovirus retinitis, pneumonia, cystitis, schistosomiasis and vaginal candidiasis. Fibrotic conditions that can be treated are pulmonary, renal and vascular fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  uteroglobin, e.g. in neonatal broncho-pulmonary dysplasia, complications of haemodialysis and inherited glomerulopathy. Uteroglobin can also be used to increase the rate of artificial insemination, in humans or animals, by treatment of sperm, fertilised eggs or embryos before transfer to the uterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat: uteroglobin; immunoglobulin A mediated disease; IgA nephropathy; autoimmune disorder; pulmonary inflammation; Wegener's granulomatosus; Goodpasture's disease; diabetic glomerulosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLOPMHKAELVKLLVQVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating and preventing inflammation and fibrosis with human uteroglobin - which inhibits phospholipase A2 and binds to fibronectin, for clinical or cosmetic use, e.g. in respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.0%; Score 85.5; DB 20; Length 75; 35.5%; Pred. No. 0.0067; Live 12; Mismatches 27; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                 Disclosure; Fig 1; 59pp; English.
(USSH ) US NAT INST OF HEALTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                 Pilon AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 22; Conserva
                                                                WPI; 1999-059777/05
                                                                                                                                                  distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 AA;
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                               Mukherjee AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
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AAB32130
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The present invention describes the use of uteroglobin in the diagnosis and prevention of IgA mediated diseases, such as IgA nephropathy, wegener's granulomatosus. Goodpasture's disease and diabetic glomerulosclerosis. This is possible as uteroglobin binds to fibronectin, preventing the complexing of fibronectin with IgA and the deposition of immune complexes in the kidney.
                                                                                                                                    Use of a composition comprising uteroglobin (or a fragment, derivative, mimetic or variant), for inhibiting or treating an immunoglobulin-A mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Streptomyces subtilisin inhibitor reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subtilisin inhibitor; protease inhibitor; human; PSTI; hPSTI.SSI; pancreatic secretory trypsin inhibitor; SSI; enzyme engineering; protein engineering; detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84..96
/label- M2_tag
/note- "affinity tag facilitates purification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 85.5; DB 21; Length 75; llarity 35.5%; Pred. No. 0.0067; Conservative 12; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..21
/label= Sig_peptide
/note= "E. col.1 phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hPSTI.SSI chimeric subtilisin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Escherichia coli strain MM294;
Chimeric Streptomyces sp.;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW26362 standard; Protein; 96 AA.
Zhang Z;
                                                                                                                                                                                                                                                                                                         Example 9; Fig 1; 60pp; English.
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69
/note= '
                                                                                                                                                                                                              Aoki A,
                                                                                                                                                                                                                                                   WPI; 1994-219093/27.
                                                                                                                                                                                    (FORS/) FORSSMANN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AA;
  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1997.
                                                                                                                                                          30-DEC-1992;
                                                                                                                                                                                                               Adermann K,
                                                                                                        07-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                             Raida M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gs
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AAW11628
ID AAW11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "When the peptide exists in dimeric form the cysteine at position 3 forms a disulfide bond with the cysteine at position 69 on the antiparallel peptide strand."
                                                                                                                                                                                             This polypeptide comprises human pancreatic secretory trypsin inhibitor (PSTI), modified to include a Streptomyces subtilisin inhibitor (SSI) reactive site. A phoA signal peptide facilitates expression in E. coli. The polypeptide is encoded by a DNA construct (AAT84524) produced by PCR amplification of overlapping synthetic oligonucleotides. Novel modified subtilisin inhibitors are claimed in which a human standard mechanism inhibitor, such as PSII, has an altered reactive site so that its dissociation constant for inhibition of subtilisin is reduced by at least a
                                                                                                                                                                                                                                                                                                                factor of 100. Also claimed are: a nucleic acid encoding the subtilisin inhibitor; expression vectors; and transformed host cells. The novel subtilisin inhibitors combine the low allergenicity of human standard mechanism inhibitors, which are not specific for subtilisin, and the high affinity of non-human subtilisin inhibitors such as SSI. They form a complex with subtilisin, so as to avoid problems of allergenicity in detergent formulations, and can also be used in affinity purification and (diagnostic) quantification of subtilisin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LLFTPSAQAAGNTGADSLGREAKCYNEDVMCPMVYDPVCGTDGNTYPNECVLCFEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lymphocytoma proliferation activating peptide; LPAP; tumour; degenerative disease; Lymphocyte; mesenchyme tissue; epidermal injury; cardiovascular disease; respiratory disease; urogenital disease; nervous system; immune system; antibody;
                                                                                                                  Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81; DB 18; Length 96; Pred. No. 0.033;
                                                     B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Indels
                                                     Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymphocytoma proliferation activating peptide (LPAP)
                                                     C, McGrath M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LVGTPEELYEGTLGKYNV-----NEDAKAAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 HKAELVKLLVQVLGSQDGAGTDYKDDDDK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR55778 standard; peptide; 70 AA
                                                                                                                                                                      Example 2; Fig 9A; 69pp; English.
                                                       Hartman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%;
28.1%;
  95US-0548186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.1 nes 25; Conservative
                           (ARRI-) ARRIS PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                              WPI; 1997-259023/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA;
                                                                                          N-PSDB; AAT84524
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                                                                                                                                               composition(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
  25-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ID AAR5
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69 forms a disulfide bond position 3 on the strand "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 FQRVIETLLMDTPSS-YEAAMELFSPDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant peptide; host cell; expression vector; hormone; antimicrobial; epitope; ACTH; VIP; GHRH; CGRP; amylin; osteocalcin; insulin; natriuretic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphocytoma proliferation activating peptide (LPAP) is used as a medicament for the treatment of disturbances in the cell growth of normal and tumour cells; degenerative diseases of humans e.g. of lymphocytes and other mesenchyme tissues; epidermal injuries; cardiovascular., respiratory- and urogenital diseases; the nerve system and the immune system. Antibodies directed against LPAP can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocytoma proliferation activating peptide structure and peptide - its prodn and its use for the treatment of, eg tumours, hypoplasia, skin-, cardiovascular-, respiratory- and urogenital-diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forssmann W, Hock D, Meyer M;
            When the peptide exists in d cysteine at position 69 form with the cysteine at positio antiparallel peptide strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79.5; DB 15;
Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Target peptide from an ubiquitin fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also be used in diagnostic assays
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27.48;
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                                                                                                                                                                                                                                                                                                                                            92DE-4244565.
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98WO-US11026.

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Mukherjee AB, Pilon AL, Zhang Z;
                                                                                                         (USSH ) US NAT INST OF HEALTH
                                                                                        (CLAR-) CLARAGEN INC.
                                                                                                                                                                                           WPI; 1999-059777/05.
    28-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uteroglobin; phospholipase A2; fibronectin; inflammation; asthma; cystic fibrosis; premature labour; infertility; rheumatoid arthritis; type I diabetes; nephropathy; inflammatory bowel disease.
Crohn's disease; ulcerative collitis; pancreatitis; peritonits; allergy; multiple organ failure; adult respiratory distress syndrome; acute renal failure; organ transplant rejection; autoimnume uveitis; corneal transplant surgery; neonatal RBS; cytomegalovirus retinitis; pneumonia; cystitis; schistosomiasis; vaginal candidiasis; fibrosis; neonatal broncho-pulmonary dysplasia; haemodialysis; glomerulopathy;
                                                                                                                                                                                                                                                                                                                                        A fermentation method has been discovered for producing a target peptide
                                                                                                                                                                                                                                                                                                                                                     from an ubduitin fusion protein. The method involves inducing the synthesis of the fusion protein. The method involves inducing the protein by a transformant contained in a fermentation culture; culturing the transformant under conditions suitable for intracellular production and accumulation of the induced fusion protein in at least 50% specific specific hydrolase to release the target peptide; and recovering the target peptide. The present sequence represents a specifically claimed example of a target peptide. The method can be used to produce e.g. peptide hormones, antimicrobial peptides, peptide epitope fragments, ACTH, VIP, GHRH, CGRP, amylin, osteocalcin, insulin, and natriuretic peptides. The system can provide recombinant fusion proteins in high specific yields of over 50% of total cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High level expression of recombinant peptide(s) - using host cells comprising an expression vector encoding a ubiquitin-peptide fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%; Score 79.5; DB 18; Length 70; 27.4%; Pred. No. 0.034; tive 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                             Yost PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human uteroglobin-like protein CC10.
                                                                                                                             Roberts SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW87569 standard; protein; 70 AA.
                                                                                                                                                                                                                                                                                                Claim 40; Page 56; 72pp; English.
95US-0553006
95US-0000822
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                                                                                                                             Lohnas GL, Pilon AL,
                                                                                                                                                                     WPI; 1997-100203/09
                                                             (IGEN-) IGEN INC. (YOST/) YOST P B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 AA;
                                                                                                                                                                                                            High level
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                        protein
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Matches
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The present sequence represents a uteroglobin-11ke protein. Recombinant human uteroglobin inhibits phospholipase A2 (PLA2), and binds to fibronectin. Inhibition of PLA2 is used to treat or prevent a wide range of systemic and ocular inflammations, asthma, cystic fibrosis, premature labour, infertility, rheumations asthma, cystic fibrosis, premature inflammatory bowel disease, Crohn's disease, ulcerative colitis, peritonitis, allergy, multiple organ fallure, adult respiratory distress syndrome (RDS), acute renal failure, inflammation secondary to infection or surgery, and organ transplant rejection. Some specified applications are in autoimmune uvelits, corneal transplant surgery, neonatal and adult RDS, cytomegalovirus retinitis, pneumonia, cystitis, schistosomiasis and vaginal candidiasis. Fibrosis. Uteroglobin may be administered to correct deficiency in endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uteroglobin, e.g. in neonatal broncho-pulmonary dysplasia, complications of haemodlalysis and inherited glomerulopathy. Uteroglobin can also be used to increase the rate of artificial insemination, in humans or animals, by treatment of sperm, fertilised eggs or embryos before transfer to the uterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; uteroglobin; immunoglobulin A mediated disease; IgA nephropathy; autoimmune disorder; pulmonary inflammation; Wegener's granulomatosus; Goodpasture's disease; diabetic glomerulosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
<del>, .</del>i
Treating and preventing inflammation and fibrosis with human uteroglobin - which inhibits phospholipase A2 and binds to fibronectin, for clinical or cosmetic use, e.g. in respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%; Score 79.5; DB 20; 27.4%; Pred. No. 0.034; tive 17; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB32128 standard; protein; 70 AA.
                                                                                                                                                                                                   Disclosure; Fig 1; 59pp; English.
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Matches 17; Conservative
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                                                                                                                          distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AA;
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artificial insemination.

Homo sapiens

03-DEC-1998

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                                                                                                                                                                                                                                                           The present invention describes the use of uteroglobin in the diagnosis and prevention of IgA mediated diseases, such as IgA nephropathy, wegener's granulomatosus, Goodpasture's disease and diabetic glomerulosclerosis. This is possible as uteroglobin binds to fibronectin, preventing the complexing of fibronectin with IgA and the deposition of immune complexes in the kidney.
                                                                                                                                                    Use of a composition comprising uteroglobin (or a fragment, derivative, mimetic or variant), for inhibiting or treating an immunoglobulin-A mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::|||: || | || : :: ::| : | :|| :| | : ::||: ::
6 FQRVIETLLMDTPSS-YEAAMELFSPDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Clara cell protein-derived antiviral peptide, SEQ ID NO:118.
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                                                                                                                                                                                                                                                                                                                                                                                                    18.6%; Score 79.5; DB 21; Length 70; 27.4%; Pred. No. 0.034; Live 17; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB64165 standard; peptide; 91 AA.
                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Clara cell protein-derived
                                                                                                                                                                                                                              Example 9; Fig 1; 60pp; English.
                                                                                          Zhang
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2000IE-0000385
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13-APR-2000; 2000WO-US09979
                              99US-0130434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 27.4 Matches 17; Conservative
                                                                                                                                                                                                    pulmonary inflammation -
                                                                                          Mukherjee AB, Zheng F,
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                                                                                                                       WPI; 2000-687100/67.
                                                                                                                                                                                                                                                                                                                                                                       70 AA;
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18-MAY-2000;
18-MAY-2000;
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03-MAR-2000;
                            21-APR-1999;
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peptides induce functional maturation of control in thymocycles and act as during pregnancy, thus enhancing the immune system in embryogenesis.

The peptides of the invention are non-immunogenic, and function without the requirement for Clara cell receptors. The peptides are used prophylactically and therapeutically against viral infections, specifically infections caused by retroviruses, togaviruses, and particularly infections by HIV, human T-lymphocyte virus 1 (HTLV-1), HTLV-3, Raposi's Sarcoma-associated herpes virus, human herpes virus 6 (HHV-6), HHV-8, viruses of the genus Mollussippoxitus, hepatitis A, B, or c'virus, or cytomegalovirus. The peptides can also be used to reduce the likelihood of septic shock syndrome in a patient about to undergo surgery, and can be used to treat this condition in a post-operative patient. They can also reduce the likelihood of cachexia in a patient about to undergo surgery. The peptides can be used to treat autoimmune conditions such as multiple sclerosis, systemic lupus erythematosus, myasthenia gravis, rheumatoid arthritis, Sjogren's disease, ulcerative colitis, and diabetes or to ameliorate immune damage and/or disease progression. The peptides can also be used to treat encolumne colitis, and diabetes or to ameliorate immune damage and/or disease progression. The peptides can also be used to treat encolumne colitis, and diabetes or to ameliorate immune damage and/or disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-term pregnancy with respect to long-term profection against chemical carcinogens and lifetime reduction in breast cancer risk, and also inhibit prostaglandin-induced pre-term delivery. The peptides induce functional maturation of cortical thymocytes, and act as
                                                                                                                                                                                                                                                                                     The invention relates to pharmaceutical compositions comprising fragments or corresponding to human Clara cell protein fragments or conservative variants thereof (AAB64050-B6478). The peptides of the invention, unlike native Clara cell protein, have potent antiviral activity, being able to block viral replication via the inhibition of reverse transcriptase and p24 activities. The clara cell-derived proteins of the invention also have a broad immune potentiator effect and anti-infective (antibacterial and antifungal, as well as antiviral) activity. The peptides of the invention may also unduce the synthesis of inhibin, a secreted protein with tumour suppressor activity, and may also upregulate the expression of pro-apoptotic genes. The peptides may additionally mimic the effects of full-term pregnancy with respect to long term protection against
                                                                                                                 Novel pharmaceutical formulation comprising a compound that comprises a peptide isolated from Clara cell protein useful for treating autoimmune disorders, cancers, viral infections, septic shock syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progression or development of cancers such as breast cancer, colon cancer, leukaemia, brain cancer, lung cancer and melanoma. The present sequence represents a human Clara cell protein-derived peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 79.5; DB : Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
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                                                                                                                                                                                                                                         Claim 1; Page 129; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%;
27.4%;
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                                                                     WPI; 2001-146767/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence of the invention.
                    Prendergast PT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                              cachexia
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AAW26363
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36 DGNTYPNECVLCFEG----RKRQTSILIQKSGPCGGGGSDYKDDDDK 78
                                                   RESULT 14
     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises human pancreatic secretory trypsin inhibitor (PSTI), modified to include a turkey ovomucoid third domain (OWTKY3) reactive site. It is encoded by a DNA construct (AAT84525) produced by PK amplification of overlapping synthetic cliqued in which a human standard mechanism inhibitors are claimed in which a human standard mechanism inhibitor, such as PSTI, has an altered reactive site so that its dissociation constant for inhibition of subtilisin is reduced by at least a cate or of 100. Also claimed are: a nucleic acid encoding the subtilisin inhibitor; expression vectors; and transformed host cells. The novel subtilisin inhibitors combine the low of specific for subtilisin, and the high affinity of non-human subtilisin, so as to avoid problems of allergenicity in detergent formulations, and can also be used in affinity purification and complex such as observed in affinity purification and constant and an also be used in affinity purification and constant and an area of a subtilisin.
                                                                                                                                                                                                                                                                                                                                                                    /label- M2_tag
/note= "affinity tag facilitates purification"
                                                                                                                                                                                                                                                                                                                     /note= "turkey ovomucoid third domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent composition(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 76.5; DB 18; Length 78; 35.4%; Pred. No. 0.092; tive 5; Mismatches 21; Indels :
                                                            Subtilisin inhibitor; protease inhibitor; human; PSTI; hPSTI.OWTKY3; pancreatic secretory trypsin inhibitor; turkey ovomucold third domain protein; enzyme engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGrath M,
                               hPSTI.OMTKY3 chimeric subtilisin inhibitor.
                                                                                                                                                                                                                                                                                                                                         reactive site"
                                                                                                                                                                                                                                          /label- Sig_peptide
                                                                                                                                                                                                                                                                          /label- Mat_protein
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hartman C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 10A; 69pp; English.
                                                                                                                                                                                                                                                                                            22..31
/label= OMTKY3
                                                                                                                protein engineering; detergent.
                                                                                                                                          Chimeric Homo sapiens;
Chimeric Meleagris gallopavo;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US17153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0548186
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARRI-) ARRIS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Estell DA, Fisher J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-259023/23.
N-PSDB; AAT84525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA;
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02-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                          Peptide
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This polypeptide comprises human pancreatic secretory trypsin inhibitor (PSTI), modified to include a Streptomyces subtilisin inhibitor (SST), mutated reactive site. It is encoded by a DNA construct (AAT64526) produced by PCR emplification of overlapping synthetic oligonucleotides. Novel modified subtilisin inhibitors are claimed in which a human standard mechanism inhibitor, such as PSTI, has an altered reactive site so that its dissociation constant for inhibition of subtilisin is reduced by at least a constant for inhibitor; expression vectors; and transformed host calls. The novel subtilisin inhibitors expression vectors; and transformed host calls. The novel subtilisin inhibitors sundard mechanism inhibitors, which are not specific for subtilisin, and the high affinity of non-human studies and as SSI. They form a complex with formulations, and can also be used in affinity purification and diagnostic) quantification of subtilisin.
                                                                                                                                     Subtilisin inhibitor; protease inhibitor; human; PSTI; hPSTI.SSI; pancreatic secretory trypsin inhibitor; SSI; enzyme engineering; protein engineering; detergent.
                                                                                                                                                                                                                                                                                                                                          22..32
/label- SSI
/note- "Streptomyces subtilisin inhibitor mutated
                                                                                                                                                                                                                                                                                                                                                                                       reactive site contains Ala at P6, Ala at P5, Ala at P4, Leu at P1 and Arg at P3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- M2_tag
/note- "affinity tag facilitates purification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent composition(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt
                                                                                                        hPSTI.SSImutant chimeric subtilisin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McGrath M,
                                                                                                                                                                                                                                                                                            /label- Sig_peptide
                                                                                                                                                                                                                                                                                                                          'label = Mat_protein
                                                                                                                                                                                                                                                               Location/Qualifiers
                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 11A; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estell DA, Fisher J, Hartman C;
                AAW26364 standard; Protein; 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0548186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US17153.
                                                                                                                                                                                                     Homo sapiens;
Streptomyces sp.;
                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-259023/23.
N-PSDB; AAT84526.
                                                                                                                                                                                                Chimeric Homo sapier
Chimeric Streptomyce
Chimeric synthetic.
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                                            AAW26364;
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AAW26364
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Gaps 'n.

35 DAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAGTDYKDDDDK 82

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Best Local Similarity 35.4 Matches 17; Conservative

Query Match

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1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides and polynucleotides encoding the polypeptides, which are expressed in bovine mammary gland tissue, useful for stimulating mammary gland growth or function, or inducing differentiation of milk producing cells -
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to proteins derived from bovine mammary gland cells. The invention is useful for stimulating bovine mammary gland cell growth and function, inhibiting the growth of various mammary gland cancer cells, inhibiting angiogenesis and vascularization of tumours, or modulating the growth of blood vessels in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.9%; Score 76.5; DB 22; Length 102; 30.8%; Pred. No. 0.13; Live 10; Mismatches 26; Indels 9
                            Length 78;
                           Score 76.5; DB 18; Length
Pred. No. 0.092;
5; Mismatches 21; Indels
                                                                                                     36 DGNTYPNECVLCFEG-----RKRQTSILIQKSGPCGGGSDXKDDDDK 78
                                                                                  35 DAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAGTDYKDDDDK 82
                                                                                                                                                                                                                                                                                                         Bovine; mammary gland; cancer; tumour; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grigor MR, Molenaar AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD.
(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
                                                        5; Mismatches
                                                                                                                                                                                                                                                                            Bovine mammary tissue derived protein #57.
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Job time : 41.1684 secs
                                                                                                                                                                                      AAB87666 standard; protein; 102 AA
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                        17.9%;
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Best Local Similarity 30.8%
Matches 20; Conservative
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                                                        17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-226619/23.
                                            Best Local Similarity
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 78 AA;
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LGKIL 85
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Q9uigO homo sapien Q81081 human parai Q8ty89 methanopyru Q19742 caenorhabdi

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Q8vxx7 arabidopsis Q8qzr1 mus musculu Q9lvg2 arabidopsis O13450 saccharomyc O80740 arabidopsis Q9hv15 pseudomonas

08yeg5 brucella me 08ryj9 oryza sativ 08s808 borrella bu 044978 borrella bu 044978 borrella bu 055942 pyrococcus 057942 pyrococcus 057942 pyrococcus 055651 mus musculu p97789 mus musculu 097789 pyrococcus 0568122 pyrococcus 0568122 pyrococcus 058122 pyrococcus 058122 pyrococcus

Run

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.9%; Score 472; DB 4; Length 95
98.9%; Pred. No. 7.3e-45;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bingle C.D.;
"Human RYD5, a new secretoglobin.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY026938; AAR08972.1;
SEQUENCE 95 AA; 10457 MW; F629AF06C96D2392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last and Putative ligand binding protein RYD5 Homo sapiens (Human).
                            Q9UIGO
Q81081
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Q19742
Q8QZR1
Q9UXZ
O13450
Q8QZR1
Q9HVL5
Q8YCG5
Q8YC5
Q8YCG5
Q8YC
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P97790
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Best Local Similarity 98.9
Matches 93; Conservative
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Q94008 mus musculu
Q8xm24 clostridium
Q9xab8 drosophila
Q9467 oryctolagus
Q9ut83 schizosacch
Q99jz9 mus musculu
Q8qx12 sorghum mos
Q8qx11 sorghum mos
Q9fw93 oryza sativ
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                                                                                                                                                                                                             ... VQVLGSQDGAGTDYKDDDDK 104
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                                                                                                              April 28, 2003, 14:36:31 ; Search time 25.732 Seconds
               GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             671580 segs, 206047115 residues
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Listing first 45 summaries
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sp_invertebrate:*
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Q9D008
                                                                                                                                                                                       RESULT 4
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                                                                                                    Rattus rattus (Black rat).
Eukaryota, Metazoa; Chorddta; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KGSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KGSSA-LLVALTVLCICGLTRAEDDNEFFMEFLQTLLVGTPEELYEGPLGKYNVNDMAKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gutierrez-Sagal R., Nieto A.;
"Cloning and sequencing of a cDNA encoding hamster uteroglobin/clara cell 10 kDa protein.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: L37041, ALi31349.1;
-InterPro: IPR00328; Uteroglob_sub.
InterPro: IPR00328; Uteroglobin.
Promo, FO012475; Uteroglobin, 1.
Promo, F0012475; Uteroglobin, 1.
SMO0096; UTG; 1.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-FISCHER; TISSUE-OLFACTORY EPITHELIUM;
MEDLINE-92007724; PubMed-1915264;
MEDLINE-92007724; PubMed-1915264;
MORAL GENES for Dotential ligand-binding proteins in subregions of the olfactory mucosa.";
MORAL GENES for Dotential ligand-binding proteins in subregions of EMBO J. 10:2813-2819(1991).
EMBI: X60661; CAA43068.1; --
INTERPRO; IRRO00329; Uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ITWAVVMLSVCCSSASSDTCPGFFQVLEFLFWGS-ESSYEAALKFYNPGSDLQDSGTQLK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleòstomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 344.5; DB 11; Length 75.0%; Pred. No. 1.1e-30; 1ve 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10401 MW; 25A4BBBB4977E247 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AMTELKSCIDGLQPMHKAELVKLLVQVLGSQD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                Potential ligand-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 18
96 AA; 10509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, CC10 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00096; UTG;
SEQUENCE 94 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus.
NCBI_TaxID=10036;
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CC10.
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108 VD 96
10 VD 96
10 VD 96
10 VD 97
10
DDT DDT READ DT READ D
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular evolution of the Metazoan protein kinase C multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                    01-AUG-1998 (TERMBLEE) 07, Created)
01-MAR-2002 (TERMBLEE) 07, Last sequence update)
Stress-responsive protein kinase (PRKSD).
Suberites Gomnoula (Sponge).
Bukaryota, Metazoa; Porifera; Demospongiae; Tetractinomorpha; Hadromerida; Suberitidae; Suberites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.3%; Score 87.5; DB 5; Length 478; 31.0%; Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96394688; PubMed-8798342;
Kruse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
Mueller W.E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
54 kDa
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                                                                                                                      478 AA
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Best Local Similarity 31.0%; Pred. No. v.....
Watches 27; Conservative 18; Mismatches
SCIDGLQPMHKAELVKL----LVQVLGSQD 92
                              64 KLVDTLPQKTRMNIMKLSEIILTSPLCNQD 93
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                                                                                                                      PRT;
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                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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InterPro; IPR002048; EF-hand
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Q9VAB8
            DR DR DR WXW
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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Sabhurner M., Batalov S., Casavant T., A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Raxi K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wishiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 KGGGALSAVAATKSPIIFIGTGEHIDDFEPFKTQPFISKLLGMGDIEGLID-----KVN 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.2%; Score 76.5; DB 11; Length 504;
Best Local Similarity 32.4%; Pred. No. 5.4;
Matches 36; Conservative 16; Mismatches 40; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium. NCBL_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55720 MW; 79AD58BE6D1E89CA CRC64;
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EMBL; AP003188; BAB80572.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1346087; Srp54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium perfringens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA;
PROSITE; PS00300; SRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
SEQUENCE
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008XM24
AC 008XM
AC 001-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
COS 01-M
COS 02 Clos
COS 02 Clos
COS 02 Clos
COS 03 Clos
COS 03 Clos
COS 03 Clos
COS 03 Clos
COS 04 Clos
COS 05 Clos
CO
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REALINE—2019006; PubMed=10731132;

REALINE—2019006; PubMed=10731132;

Adams M.D., Celniker S.E., in Pub. Hoskins R.A., Galae R.F.,

Adams M.D., Celniker S.E., in Pub. Hoskins R.A., Galae R.F.,

RA Adams M.D., Celniker S.E., in Pub. Hoskins R.A., Galae R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Davle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Baroktein P., Brottier R.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,

RA Durbin K.J., Benose M., Dugan-Rocha S., Duno P.,

RA Durbin K.J., Bongelista C.C., Ferraz C.J., Ferriara S., Fleischmann W.,

RA Durbin K.J., Burneplista C.C., Ferraz C.J., Rerriera S., Fleischmann W.,

RA Bartis N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,

Harvey D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., May M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Mount S.M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Rander R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J. M.,

Rander K., Remington K.A., Nixon K., Nusskern D.R., Pacle J. M.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Shue B.C., Siden-Kiamos I., Sangson M., Schoeler F., Shen H.,

Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang K.,

Wang Z.Y., Wang A.M., Weinstock G.M., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterrygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, (CBI_TaxID=7227).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 EDNDEF---FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAE 79
                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                             Length 2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                 2104 AA; 236010 MW; 5FE345659599EED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 AA.
                                                                                                                                                                                                                                                                                                                             ;; Score 76; DB
;; Pred. No. 38;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 LVKLLVQVLGSQ------DGAGTDYKDDDD 103
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771 LIKLQERVLSTRPEFLIGNWIEDARTMLKDSDD 803
                                                                                                                                                                                                                                                                                                                         Score 76;
Pred. No. 3
                                                                                                                      SMART; SM00060; FN3; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
InterPro; IPR003961; FN_III.
Pfam; PF00754; FS_F8_type_C; 1.
Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                         14.2%;
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.09
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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63 KECTDEIDKGKRVLIAAVLTKIV 85

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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Glibbs R.A., Myers E.W., Woold G.W., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CICRMATGEDNDEFFMDFLQTLLVGTP----EELYEGTLG-KYNVNEDAKAAMTELKSC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CICQFSVRVPKD-----IHŢDIVGHPPVLISELVLQCIRGINYVLIEESS---TICKKC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTEL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 27.2%; Pred. No. 9.1;
Matches 28; Conservative 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.6%; Score 73; DB 6; Length 90; 27.7%; Pred. No. 1.5; Live 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LACRIMAL GLAND;
Zhao C., Nguyen T.X., Lehrer R.I.;
Zhao C., Nguyen T.X., Lehrer R.I.;
Submitted (EP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF308614; AAG42802.1; -.
InterPro; IPR000329; Uteroglobin.
Fpfam; PF01099; Uteroglobin; 1.
SMART; SM00096; UTG; 1.
SMART; SM00096; UTG; 1.
                                                                                                                                                                                                                                                                                                                                                 2F5D641877EFD97E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 IDGLQPMHKA-----ELVKLLVQVLGSQDGAGTDYKDDD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | ||:|| ||:|| | 55 CEKLARYHKGISYKEDD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 AA.
                                                                                                                                                                                                                                                                                                      PROSITE; PSO0028; ZINC_FINGER_C2H2_1; 5. PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 5. MAN-binding; Metal-binding; Zinc-finger. SEQUENCE 457 AA; 53091 MW; ZFSD64187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KSCIDGLQPMHKAELVKLLVQVL 88
                                                                                                                                                                                                                                             FlyBase; FBgn0039740; CG7928.
InterPro: IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; Z
SMART; SM00355; ZnF_C2H2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipophilin AL.
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Local Sim
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Matches
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Indels 28; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.,
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AL109739; CAB52270.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.6%; Score 73; DB 3; Length 609; Best Local Similarity 23.5%; Pred. No. 17; Matches 23; Conservative 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; DC005347, 2FFH. MGD; MGI:1346087; Srp54. InterPro: IPR003593; AAA_ATPase. InterPro: IPR00897; SRP54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to signal recognition particle 54 kDa.
                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative RNA-binding protein.
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                                                                                                        609 AA
                                                                                                                                                                                   (TrEMBLrel. 13, Created)
                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, 119339, 2SXL.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR000505; RNA_2.
Ffam: PF00076; rrm: 3.
SMART; SM00360; RRM; 2.
PR0SITE; PS00102; RRM, 2.
PR0SITE; PS001030; RRM; 2.
SEQUENCE 609 AA; 68547 MW; 0ADE
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Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1
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                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
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                                                                                              Q9UT83;
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RESULT 9
Q9UT83
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Query Match
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                                                                                                                                                                                                                                                                                                                                            Chen J., Chen J.P., Adams M.J.; "Characterisation of potyviruses from sugarcane and maize in China."; Arch. Virol. 147:0-0(2002).
                                                                                                       255 KGGGALSAVAATKSPIIFIGTGEHIDNFEPFKTQPFISKLLGMGDIEGLID-----KVN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 TGEDNDEFFMDFLQT----LLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMH 76
                                                                Gaps
                                                                                   1 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyprotein.
Sorghum mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 70.5; DB 12; Length 3071;
; Pred. No. 2.5e+02;
10; Mismatches 17; Indels 17;
                                           DB 11; Length 500;
                                                                                                                                        E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 98
                                                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COAT PROTEIN.
W; 2FD59A0668DE2FB7 CRC64;
        UNKNOWN_1.
2 MW; C957B6F76C6A224B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    P1 PROTEIN.
HC-PRO PROTEIN.
P3 PROTEIN.
6K1 PROTEIN.
C1 PROTEIN.
6K2 PROTEIN.
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NIA-PRO PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3071 AA
                                                                                                                                                                                                     PRT; 3071 AA
                                       13.5%; Score 72.5; C
32.4%; Pred. No. 15;
Live 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIB PROTEIN
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                                                                                                                                                                                                                           Created)
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                      55492 MW;
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                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                       Query Match 13.5%
Best Local Similarity 32.4%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.19
Best Local Similarity 33.39
Matches 22; Conservative
SMART; SM00382; AAA; 1.
PROSITE; PS00300; SRP54;
SEQUENCE 500 AA; 55492
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                                                                                                                                                                                                     PRELIMINARY;
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2750
3071
                                                                                                                                                                                                                                                       Polyprotein.
Sorghum mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                     500 AA;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        Potyvirus.
NCBI_TaxID=32619;
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NCBI_TaxID=32619;
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                                                                                                                                                                                                                                                                                                                                  STRAIN-XIAOSHAN;
                                                                                                                                                                                                                                                                                                                                                                  Arch. Virol. 14
EMBL; AJ310197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 KAELVK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                 "Characterisation of potyviruses from sugarcane and maize in China."; Arch. Virol. 147:0-0(2002).
EMBL; AJ310198; CAC84438.1;
                                                                                                                                                                                                                                                                                                                                                   17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        TGEDNDEFFMDFLQT----LLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTP---EELYE-----GTLGKY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KAELVKLLVQVLG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                   Length 3071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 643;
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                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                              COAT PROTEIN.
MW; E3D326DE1B9ACB05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRINTS, FACOLOGY, FACOTROME_P450; UNKNOWN_1.
HEMBE, MONDOXYGENSE, OXIGOREDUCTASE.
SEQUENCE 643 AA; 70706 MW; C695CA5DF1A36463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative cytochrome P450.
OSJNBA0026112.20.
                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                            2363 TGKKKD-YFMDFSDTDKEEILKQSCERLYEGQLGVWNGSLKAE-
                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.5e+02;
10; Mismatches 17
                                                                                    P1 PROTEIN.
HC-PRO PROTEIN.
P3 PROTEIN.
6K1 PROTEIN.
                                                                                                                                                                                                          NIA-VPG PROTEIN.
NIA-PRO PROTEIN.
NIB PROTEIN.
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                                                                                                                                                                                                                                                                                                                   Score 70.5;
                                                                                                                                                                         CI PROTEIN.
6K2 PROTEIN.
                  STRAIN=YUHANG;
Chen J., Chen J.P., Adams M.J.;
                                                                                                                                                                                                              , 47
2229
2750
3071
349537 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                   13.1%;
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                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 33.3
Matches 22; Conservative
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                                                                                                                                                                                                                                                              2751 307
3071 AA;
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Matches 33; Conserv
SEQUENCE FROM N.A.
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Best Loca
Matches
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A MCMAK-Thompson B. Chaney N., Wing J.S., Gould S.J., Loper J.E.;

"Characterization of the pyoluteorin biosynthetic gene cluster of genedomonas fluorescens Pf-5.";

"J. Bacteriol. 181:2166-217(1999).

EMBL; AF081920; AAC38075.1; -...

In InterPro; IPR00127; Ac_transferase.

InterPro; IPR00127; Ac_transferase.

InterPro; IPR00127; Ac_transferase.

InterPro; IPR00199; Retoacyl-synt.

InterPro; IPR00199; Retoacyl-synt.

InterPro; IPR00199; Retoacyl-synt.

R Pfam; PF00380; Acyl-transf; 1.

R Pfam; PF00380; Acyl-bynt. 2.

R Pfam; PF00380; Pp-binding; 2.

R PROSITE; PS00006; B_KETOACYL_SYNTHASE; 2.

R PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.

R PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.

R PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.

W PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.

R PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.

W PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nowak-Thompson B., Gould S.J., Loper J.E.;
"Identification and sequence analysis of the genes encoding a polyketide synthase required for pyoluteorin biosynthesis in Pseudomonas fluorescens Pf-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Fibronectin-binding protein.
rNGB OR LL1327
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
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                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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; Pred. No. 2.4e+02;
14; Mismatches 19;
                                                                                                                                                                                                                                                                               2458 AA
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                                                                                                                                   416 RDEKEWEKPMEFMPERFLPGGDGEGVD 442
                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                90 SQ-----DGAGTD 97
                                                                                                                                                                                                                                                                             PRT;
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MEDLINE-99194726; PubMed-10094695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE-98094250; Pubmed-9434161;
                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, Polyketide synthase type I.
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Best Local Similarity 32.1%;
Matches 17; Conservative 1
                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 204:17-24(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas.
NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                             051827
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                                                                                                                                                                                                                      RESULT 14
051827
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Q9CFY4
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MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
Melsenbach J., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006365; AAK05425.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 DNDEFFM---DFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQP-MHKAE 79
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                540 AA; 61285 MW; 4DAC3CCCBCF72867 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             / Match 12.8%; Score 69; DB Decal Similarity 30.6%; Pred. No. 41; nes 22; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 28, 2003, 14:43:30 Job time: 26.732 secs
                        Streptococcaceae; Lactococcus.
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                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 540 AA;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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